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-MODELE frame+ pin.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10020095/runat_15012004_163822_18707/app_query.fasta_1.1607
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg= -MINMATCH=0.1 -LOOPEI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK*100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: gb_ba:
2: gb_htg
3: gb_in:
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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1 MQGPPLLTAAHLLCVCTAAL.....HSSVIFIFCFKLLYFMELWL 1428
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29: em vi:*
30: em htg hum:*
31: em htg inv:*
32: em htg other:*
33: em htg pln:*
34: em htg pln:*
35: em htg pln:*
36: em htg mam:*
37: em htg am:*
39: em htg mam:*
40: em btg mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44		42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	. 25	24	23	22		20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	ű	4.	ω	2	ם	NO.	Result
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ALIGNMENTS

BASE COUNT 1296 ORIGIN Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB: US-10-020-095-4 (1- Qy	CDS	AUTHORS TITLE JOURNAL FEATURES source	AX537610 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
1 G-1 G-1 4	/mol type="genomic DNA" /db_xref="taxon:9606" 1,4335 1,4335 /mote="junnamed protein product"	Schuh, A. and Ouwehand, W. Diagnosis and treatment of blood disorders. Patent: WO 02070738-A 1 12-SEP-2002; Schuh, Andre (CA) Location/Qualifiers e /organism="Homo sapiens"	
& \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	P & 8	B & B &	. DD Q2 DD Q2 DD Q4 DD Q
		101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr	

1121 MEGGINFRETEPVALSEFEETGINSET/YSLEWSETASBSETITDGINFROATGSETLEU 1140 3361 ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTG 3420		761 GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal 780
101 SerProLyBA.alyBG1UA.aLeuAsnMetLeuThrTrpArgAlaG1UGLIG1UGLYG1Y	p 64	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAgnLeuProTyrSerVallleArg 760
UB1 ArgG.ly11eSerAspAsnTyrThrLeuAlaLeu11eThrTyrAlaLeuSerSerValIGly) B &	721 ValalaThrGlyPheVallleSerGluAspLeuGlyLeuThrThrThrThrProVal 740
061 LysTyrGlnDroAsnIILeAspValGlnGluSerILeHisPheLeuGluSerGlupheSer	5 B 8	701 MetGlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 720
41 GIYASHLY8SSEPROVAITHELEUTHEALATYTIEVAITHESEELEUGIYTYEARG	д b 07	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn 700
21 GlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly	Qy Db	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu
1001 ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis 1020 	Db Qy	641 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 660
AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1 	D QY	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640
61 TyrGlaArgGluLeuLeuTyrGlaArgGluAsgGlySerPheSerAlaPheGlyAsnTyr	Qy	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620
41 LysLysLysCinLeuThraspAsnLeuLysCiuLysAlaLeuSerPheMetArgGlnGly 	Ωy	581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600
CysGlyGluGlnAsnMetileAsnPhealsProAsnIleTyrIleLeuAspTyrLeuThr 9	Ωу	561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580
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SerPheSerPheProProAsmThrValThrGlySerGluArgValGln1leThrAlaIle	, Db	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540
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41 AlaSerAspAlaValThrGlimMetileLeuValLysAlaGluclyIleGluLysSerTyr 	Db	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500
ProlleArgProThrHsBeuclyGluIleProlleThrValThrAlaLeuSerProThr	p &	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480
AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe	B &	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460
LysValllelleGlulysSerAspLysbheAspIleLeuMetThrSerSerGluIleAsn	Db .	421 ThrValProGlnSerGlyThrPheLygIleGluPheProIleLeuGluAgpSerSerGlu 440
		1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT

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Cd109 nucleic acid molecules polypeptides and methods of Patent: WO 02070696-A 1 12-SEP-2002; Schuh, Andre (CA), Sutherland, Robert D. (CA)
Location/Qualifiers
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Allgument Scores:			
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Score:	7326.50	Matches:	1427
t Si	98.82%	Conservative:	1
ξ.	98.75%	Mismatches:	0
	99.71%	Indels:	17
DB:	6	Gaps:	۲

US-10-020-095-4 (1-1428) x AX534934 (1-4761)

100	81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100	81	S
352	GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT	293	뫄
80	61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80	61	Ş
292	233 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 292	233	ДĎ
60	AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60	41	Ş
232	GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA	173	뫄
40	21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40	21	2
172	ATGCAGGCCCACCGCTCCTGACCGCCGACCTCTCTGCGTGTGCACCGCCGCGCTG	113	망
20	1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu 20	_	Ş

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441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460	421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440 	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420 	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400 	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380 	341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340 	301 ABNVAlMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300 	261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle 280 	241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260 	221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240 	201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220 	181 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProlle 200 	161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180 	141 LysProLysGlnGluValLysPheArglleValThrLeuPheSerAspPheLysProTyr 160 	121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140 	101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120	
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GlyIleProIleMetArgTrpLeuSerA GAATCCCAATTATGAGGTGGCTAAGCA	AspIleGluValAlaAlaTyrAlaLeuL 	MetGlnPheTrpValSerSerGluSerLy 	SerProLysAlaLysGluAlaLeuAsnM AGTCCTAAAGCGAAGGAAGCTTTGAATA	ArgGlyIleSerAspAsnTyrThrLeuA agaGGAATTTCAGACAATTATACTCTAG	LysTyrGlnProAsnIleAspValGlnGl	GlyasnlysSerProValThrLeuThrA 	GlnLysSerAsnGlyGluPheTrpAspP cagaaatCcaacggtgaattttgggatc	ProTyrIleAspIleAspGlnAsnValL	CAG CAG	TyrGlnArgGluLeuLeuTyrGlnArgG TACCAGAGAGACTTCTCTATCAGAGGG	LysLysLysGlnLeuThrAspAsnLeuL 	CysglyGluGlnasnmetIleasnPheAi 	GlyAspValLeuGlyProSerIleAsnG	SerPheSerPheProProAsnThrValT	SerGInSerIleLeuLeuAspLeuThrA TCACAATCCATCTTATTAGACTTGACTG	AlaSerAspAlaValThrGlnMetIleL	ProlleargProThrHisLeuGlyGluI CCATCAGGCCAACACATCTGGGAGAAA
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AP410459 5883 bp mRNA linear PRI 02-MAR-2002 Homo sanions CD109 (CD109) mRNA. complete cds.	AACTTTGGC	MetGluLeuTrpLeu 1428	CAGGCTC	SerGlySerHisHisHisSerSerValIlePheIlePheCysPheLysLeuLeuTyrPhe 1423	CTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 4372	cCysAspLeuCysSerAspVa	ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG 4312	IleValAspTyrTyrGluProArgArgGlnAlaValArgSerTyrAsnSerGluValLys 1383	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4252	ValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSer 1363	GAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT 4192	GluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCys 1343	TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG 4132	LeuSerGlyPheMetValProSerGluAlaIleSerLeuSerGluThrValLysLysVal 1323	GTGTGTACAAGCTTTTCGGGCCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA 4072	ValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeu 1303	TTTGATTTAGATGTTGCTGTAAAAGAAAAATAAAGATGATCTCAATCATGTGGATTTGAAT 4012	PheAspLeuAspValAlaValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsn 1283	TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAATCAAGAAGCC 3952	TyrAsnVallysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla 1263	ATGGCAGTTAATATTTCCGCCAAATGGTTTTGGATTTTGCTATTTGTCAGCTCAATGTTGTA 3892	MetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValVal 1243	CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA 3832	LeuAlaValValGlnPro 1223	GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTT 3772	GluArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro 1217	ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA 3712	ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr 1200

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF410459 5883 bp mRNA linear Homo sapiens CD109 (CD109) mRNA, complete cds. AF410459 AF410459.1 GI:19071208

REFERENCE AUTHORS TITLE Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5883)
Lin,M., Sutherland,D.R., Horsfall,W., Totty,N., Yeo,E., Nayar,R.,
Wu,X.F. and Schuh,A.C.
Wu,X.F. and Schuh,A.C.
Cell surface antigen CD109 is a novel member of the alpha(2)
macroglobulin/C3, C4, C5 family of thioester-containing proteins
Blood 99 (5), 1683-1691 (2002)

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Wu,X.-F. and Schuh,A.C.
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                                AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG
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GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArg	ValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal 	MetGlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 	GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn 	AlaGluargPheMetGluGluasnGluGlyHisIleValAspIleHisAspPheSerLeu 		621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640 	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620 	581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600 	561 LeuTyrTrpSerLygValLygAlaGluProSerGluLygValSerLeuArgIleSerVal 580 	GluileileSerAspValleuLysileProValGlnLeuValPheLysAsnLysileLys 	ProGluasnSerTrpThrProLysalaCysVallleValTyrTyrIleGluaspAspGly 	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520 	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500 	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480 	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460	421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440	
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                                                                                                                                                                                                               MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu
AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
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VTORNVTEYKGGSNSGNGKMEAVOKINVTUPQSGTFKIE FILDSSELQLKAYFLGS
KSSMAVHSLFKSPSKTY I QLKTRDENI I KVGSPFELVVSGNKRLKELSYMVVSRGQLVA
VGKQNSTMFSLIFENSMTPKACVIVYX IEDDGEI I SDVLKI I PVQLVFKNEIKLYNGKY
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MFMNS FRAVPOECGLWVLTDANLIKOD Y I DOVUNAS PREMERIEGH I VDI HDFSLGS
SPHVRKAFPETWI I LLDTURMSKRI YQEEPSTVDDS I TSWAATGFV Y SEDLGLGLITTIPV
ELQAFQPFFI FLNLPYSV I RGEEFALE I TI FNYLKDATEVKVI I EKSDKFD I LMTSNE
I NATGRIQOTLLVFSEDGATVLFP IR FTHLGE I P I TVTALSPTASDAVTONLLVKARGI
EKSYSQS ILLDLTDNRLQSTLKTLSFSF PPNITVTGSERVQ I TAIGDVLGPS I NGLASL
I RMPYGCGGEQNNI NFAENI Y I LDYLTKKKQLTDNLKEKALSFMRQOYQRELLY QREDG
SFSAFGNYDDESGSTMLSAFVLRCFLEADPY ID LDQNULHFYTYFNLKGHOKSNGEFNDP
GRVIH SELQGGNKS PVTLTAY I VTSLLGYRKYQPNI DVQES I HFLESEF SRG I SDNYT
LAALITYALSSVGS FKAKEALMULTMRARD GDEGGNQFWSDLSEFAALMNTERTN
I QVTVTGPSS BSSVKEL DTHNRLLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTN
I QVTVTGPSS BSSVKEL DTHNRLSRQRNSLGGFASTQDTTVALKALSEFAALMSVNL
VXASGGSRRRRSI QNQEAFDLDVAVKENKDDLMHVDLAVCTSFSGGRGGRGMALMSVNL
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KTSLNILIK MPKSNLIOQMLSQOSDLGVISKTPOLESHPILGDMSIQVQVNNDQTYYQS
FQVSBYVLFKFEVTLQTFLYCSMNSKHLINGTITAKYTYGKFVKGDVTLIFLFLSFYKK
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/mol_type="genomic DNA"
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LeuThrTrpArgAlaGluGlnGluGlyGly 1	1061 LysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer 1080	3113 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3172 1021 GlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly 1040	993 TACCAGAGAGAÁCTTCTCTATCAGAGGGAAAGATGGCTCTTTCAGTG 981 ASPPXOSETG1YSETThTTTPLEUSEXALAPHEVALLEUAYGCYSF	2873 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTTACATTTTAGATTATCTGACT 2932 941 LysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGly 960	901 GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 911 GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 813 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 921 CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr	861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 880	2453 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTGCTAATGACTTCAAATGAAATAAAT
RESULT 5 AX537612 AX537612 AX537612 AX537612 AX537612 AX537612 AX537612 AX537612 VERSION AX537612 VERSION AX537612.1 GI:25269535 SOURCE Homo sapiens (human) ORGANISM Homo sapiens CREANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy 1404 SerGlySerHisHisHisSerSerValllePheClePheCy8PheLy8LeuLeuTyrPhe 1423	1364	1324 GluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCys	1284 ValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeu	Qy 1244 TyrasnValLysAlaSerGlySerSerArgArgArgArgArgSerIleGlnAsnGlnGluAla 1263	Qy 1218	Qy 1161 GlylleProlleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSer 1180

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Qy 461 LysSerPro	100 Qy 441 100 Db 1321	80 Qy 421 B0 Db 1261 240 Db 1261	60 Qy 401 180 Db 1201	40 Qy 381 40 Db 1141	20 Qy 361 20 Db 1081	Oy 341 AsnValPhe Db 1021 AATGTGTTC	Oy 321 ValGluIle Db 961 GTAGAAATT	Qy 301 AsnValMet	Qy 281 Db 841	Oy 261 Db 781	Oy 241 Db 721	Qy 221 Db 661	Оу 201 Db 601	Qy 181 Db 541	Qy 161 Db 481		_	Qy 121 ArgLeuSer Db 361 CGCTTATCA	DD 301 ATTTATGAG
SerLys	LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal 	ThyValProGinSerGlyThrPheLyBileGluPheProlieLeUGluAspSerSe	erclySerAnnSerclyAsmGlnLysMetGluAlaVaIGlnLysIleAss	ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu	LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu	AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 	ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 	AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro	ThrLysThrPheLys leAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 	LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysLysAsnIle	MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal	ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 	LeuGlyAspTrpSerI1eGlnValGlnValAsnAspGlnThrTyrTyrGlnS 	SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeu TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTA	LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 	AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAG	3GlnGluValLysPheArg	ArgieuSerPheGluThriysArgileSerValPheIleGluThAspLysAlaleuTy	ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC

1181 ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr		821 ProIleArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThr 840 	8
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) B &	781 LysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsn 800 	유 왕
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	} B &	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArg 760 	B 8
) p 4	721 ValalaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrFhrProVal 740 	유 성
	? B &	701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 720 	음 성
	5 &	681 GlySerSerProHisValargLysHisPheProGluThrTrpIleTrpLeuAspThrAsn 700 	용 성
	D 4	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680 	유 성
	; B &	641 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 660 	B 8
	, p	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640	음 경
	P &	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620 	B &
21 4	? B &	581 ThrGlnProAspSerIlevalGlyIlevalAlavalAspLysSerValAsnLeuMetAsn 600 	용 성
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                                      Schuh, A. and Sutherland, R.D.
Cd109 nucleic acid molecules polypeptides
Patent: WO 02070696-A 3 12-SEP-2002;
Schuh, Andre (CA); Sutherland, Robert D.
                                                                                                              Homo
                                                                                                                                                      Sequence 3 from AX534936
                                                                                                  Eukaryota;
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                                                                                           Mammalia;
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                                                                                                                                                                                                                  MetGluLeuTrpLeu
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|TGGAACTTTGGCTG
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                              Location/Qualifiers
          organism="Homo sapiens"
_type="genomic DNA"
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Primates;
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Catarrhini;
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VTQRNYTEYMSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGS
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SPHVRKHFPETWIMLDTNMGSRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPV
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KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI
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Matches:
Conservative:
Mismatches:
Indels:
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1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe AsnValThrIleG1yValGluLeuLeuGluHisCysProSerGlnValThrValLysAla AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGCCCACCGCTCCTGACCGCCCCCCCCCCTCTCTGCGTGTGCACCGCCGCGCTG AATGTGACTATTGGGGGGGGGGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 120 532 140 472 412 100 352 80 292 60 232 40 172

861 SerGinSerIleLeuLeuAspLeuThrAspAsnArgLeuGinSerThrLeuLysThrLeu 880	- 29	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520
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ProlleArgProThrHisLeuclyGluIleProIleThrValThrAlaLeuSerProThr 	å S	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480
	Qy dd	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460
LysVallleIleGluLysSerAspLysPheAspIleLeumetThrSerSerGluIleAsn 	A da	ω—⊨
	g Q	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420
	рь	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400
	D 5	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380
	D Q	341 AgnValPhePheLygGlnHisAgpTyrTleIleGluPhePheAgpTyrThrThrValLeu 360
GJYSerSerProHisValArglysHisPheProGlUThrTrpILeTrpLeuAspThrAsn 	, B &	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
AlaGluArgPheMetGluGluAsnGluGlyHisTleValAspIleHisAspPheSerLeu	, B &	301 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320
41 LeuThrAspA.LaAsnLeuThrLysAspTyrILeAspGLyValTyrAspAspAlaGluTyr	B &	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnĀspGluGluMetLys 300
21 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 	Db Qy	261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsmIle 280
01 Ala 13 GCC	ρρ	241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260
ACA Thr	Db Qy	221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240
93 CT	B Q	201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220
41 G1 	Db Qy	181 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIle 200
21 Pr 	Db QY	161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180
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CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGCTGCTACAGCCA
                                   SerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGly
                                                                                                                                                                                                                                                       LysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer
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Val 1243 GTA 3892	Qy 1224 MetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValVal

161 LysThrSer 593 AAAACCTCT	141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr	121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 	Qy 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120 	Oy 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100	Qy 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80	Qy 41 ABnValThrIleGlyValGluLeuGluHiBCyBProSerGlnValThrValLyBAla 60	Qy 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40	Qy 1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu 20	US-10-020-095-4 (1-1428) x AX534940 (1-5895)		nment Scores: No.: 10 No.: 117.50 Matches: 2317.58 Conservative:	BASE COUNT 1708 a 1174 c 1241 g 1772 t ORIGIN	VKASGSSRRRSI QNGEAFDLDVAVENKDDLNVOLVKOSSGORGKNALMEVNI LSGFMVPSEAI SLSETVKKVEYDHGKLNLYLDSVNETQFCVNI PAVRNFKVSNTQDAS VSI UNIVYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVI FI FCFK	GRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISDNYT LALITYALSSVGSPKAKEALMMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAA YALLSHFLQFGTSEGIFIRWILSRQRNSLGGFRSTDOTTVALKALSSFAALMMTERTN IQVTVTTGSESSSENKFIFTTPTUBLIIQFTTPALKTSTSANGGESTGGVANTYN	INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAEGI EKSYSQSILLDLTDNRLQSTLKTLSPSFPNTVTGSERVQITAIGDVLGBSINGLASL IRMPYGCGEQMINFAPNIYILDYLTKKKQLTDNLKEKALSPMRQGYQRELLYQREDD SFSAFGNYDDSGSTWISSFUIFCFIRADDVTTOTTVTWIKTGATKGNGEFWID	KAESSKVSLRISVTQPDSI YGI VAVDKSVVILMASSDI TYMENVYHELELXNTGYYLG MFMNSFAVFQECGLWYLTDANLTKDY I DGYYDNAEYAER FMEENEGHI VD I HDFSLGS SPHVEKHFPETWI WLDTNMGSRI YQBFEVITVPDSI TISWVATGFVI SEDLGLGLTTTPV ELQAFQPFFI FLNLPYSVI RGEEFALEITI FNYLKDATEVKYI I EKSDKFDI LMTSNE	SRNYSTNYFFKOHDY I IEFDYTTYLKPSLAFTATYKYTRADGNOLTLEBERNNYVIT VTORNYTEYWSGSNSGNOKMEAVOKINYTYPOSGTFKIEPPILEDSSELOLKAYFLGS KSSMAYHSLFKSPSKTYIOLKTRDENIKVOSPFELVVSGNKRLKELSYMYVSRGOLVA VGKONSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYMSKV	ELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKDY KTSLNILIKDPKSNLIQQMLSQQSDLGVISKTFQLSSHPILGDMSIQVQVNDQTYYQS FQVSEVVLPKEEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTPLLPLSFMGK KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI
Qy 521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540	Qy 501 ValSerArgGlyGlnLeuValAlaValGlyLyBGlnAsnSerThrMetPheSerLeuThr 520	Qy 481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	Qy 461 LysSerProSerLysThrTyrIleGInLeuLysThrArgAspGluAsnIleLysValGly 480	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 46	Qy 421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440	Db 1313 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	381 ThrLeuGluGluArgArgAsnNanValValIleThrValThrGluArgAsnTyrThrGlu 4	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 3	1133 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTTGATTATACTACTGTCTTG 1	341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 3 	Qy 301 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320	Qy 281 ThrLysThrPheLys1leAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300	Qy 261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnIle 280	Qy 241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260	Qy 221 ValserGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240	LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPh 	Qy 181 SerGlnGlnSerAspLeuGlyValIleSerLy8ThrPheGlnLeuSerSerHisProTle 200

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Db 8:	Оу 2.	Db 7:	Qy 2	7 dd	Qy 2	Db 6	ον 1:	Db 5	0γ 1.	Db S	. Qy 1	Db 4	0у 1	Db 4	0у 1	ΩЬ 3	Q	Db 2	Qy	Db 2.	Q	Db 1'	Qy	 Q	US-10-020-0	DB:	Query Match	Percent Sim	Pred. No.:	ORIGIN	BASE COUNT				

KAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLG
MEMNSFAVFQECCLWYLTDAKILTKDYIDGVYDNAEYAER FMEENEGHIVDIHDFSLGS
SPHVRKHFPETWIMLDTINMGYRIYQEFEVTVPDSITSWAFTGFVISEDLGLGLTTTPV
ELQAFQPFIFILNLFYSVIRGEEFALEITIFNYLKDATEVKVIIEKSBKFDILMTSNE
INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAEGI
EKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTYTGSERVQITALGDVLGPSINGLASL
IRMFYGCGEQNMINFAPNIXILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDG
SFSAFGNYDFSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDD
GRVIHSELQGGNKSPTLTAYIVTSLLGYRKYQVFRI"

83	Оу 24	Db 77	3 1	Qy 20		Οy 16 Db 59	Db 53	4.	12	Db 41	3 5	0у 8	Db 29	, 23	44	Db 17	Оу 2	Db 11	ş	US-10-020-09	Alignment Scc Pred. No.: Score: Percent Simil Best Local Si Query Match: DB:	BASE COUNT ORIGIN
3 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 89	1 MétAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLys	21 VALSETGLUYFYALLEUFTOLYSFREGLUVALTHITLEUGHTINTFFTOLEULYTCYSSET 240 [1]		01 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220 	1 Cordingingories on Civil all acort weak-randon longer cordination and	61 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180	33 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC 592	3 CECTTATCATTTCAGACCAAGACAAATATCTGTCTTCATTCA	1 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 14	13 ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC 472	3 GAAAAAGGCTCTTTTAAGACACTTACTTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 41	1 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 1	61 GIULGULGUNYSINTALASETASHLGUNTTVALSETVALLGUGLUHALAGUUGLYVALPHG 80	3 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 2	1 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 6	73 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA 232	ï	13 ATGCAGGGCCCACCGCTCCTGACCGCCGCCCCCCTCCTCTGCGTGTGCACCGCCGCGCGCTG 172	etGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAla	95-4 (1-1428) x AX534942 (1-3535)	Cores: 0 Length: 3535 5470.00 Matches: 1062 ilarity: 100.00% Conservative: 1 Similarity: 99.91% Mismatches: 0 74.44% Indels: 0 Gaps: 0	1108 a. 675 c. 731 g. 1021 t

	:CATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAAT(.eThrMetGluAsnValValHisGluLeuGluLeuTyr)	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	ωp	541 GluileileSerAspValLeuLysileProValGlnLeuValPheLysAsnLysileLys 560 	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540 	alaValGlyLysGlnAsnSerThrMe 3CTGTAGGAAAACTAAAATTCAACAAT	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500 	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480 	441 LeuGlnLeuLyBAlaTyrPheLeuGlySerLyBSerSerMetAlaValHiBSerLeuPhe 460 	421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440 	401 TyrTrpSerGlySerAbnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420 	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400 	LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 	AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 	IleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 	01 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 3 	81 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 3	261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAssnIle 280
Db 2993 TACCAGAGAGAACTTCTCTTATCAGAGGGAAGATGGCTCTTTCAGTGCTCTTTTGGGAATTAT 3052 Oy 981 AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1000	961 TyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyr	Qy 941 LysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGly 960		901 GLYASDVALLEUGLYPTÖSETILAASMGLYLEUALASETLEULLEAGMEEPTÖTYTELY	881 SerpheSerpheProProAsminrYalinzdyServiuArgyalGln1leInralalle	861 SerGinSerIleLeuLeuAspLeuThrAspAsnArgleuGInSerThrLeuLysThrLeu	41 AlaserAspAlavalinesinesileusuvallyskalasuvalyllesiulysserly:	821 ProlleArgProThrH1sLeuGlyGluileProlleThrValThrAlaueuSerProThr	801 AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAagGlyAlaThrValLeuPhe	/81 L/99/8111E11E5.111/98/81/818/D/98/108/91/108/81/108/81/108/81/98/81/108/81/98/81/98/98/98/98/98/98/98/98/98/98/98/98/98/	761 GJVG1UGLUPheAlaLeuGLUIIeThrIlePheAsnTyrLeuLysAspAlaThrGluVal	741 GluLeuGLnAlaPheGluProPhePheIlePheLeuAsnLeuProTysSerVallleArg	721 ValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal	Qy 701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThr6erTrp 720	SerProHisValArgLy9HisPheProGluThrTrpIleTrpLeuAspThrAsn 	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 	Qy 641 LeuThraspalaasmLeuThrLysAspTyrIleAspGlyValTyraspAsmalaGluTyr 660	T.euGlyMetPheMetAsnSerPheAlaValPheGLnGluCyGJyLeuTrpVal

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Alignment Sc Pred: No.: Score: Percent Simi Best Local S Query Match:	BASE COUNT	. CDS	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUTCE	AX534944 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	
ment Scores: . No.: . No.: strain arity: . Local Similarity: / Match:	1107 a	2011270	Mammalia 1 Schuh, A. Cd109 nu Patent: Schuh, I	AX534944 Sequence AX534944 AX534944. Homo sapi	053 001 113 113 021 173 041 233 061
0 5461.00 99.91 99.81 74.32	/DECUTION / 256.1. / Charletin_le="CAUS / 256.1. / Charletin_le="MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGI IRPGGNVTI / CTAINS ation="MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGI IRPGGNVTI GVELLEHCPSQOTVKAELLKTASNLTWSVFLEXDEWERGSFRTLTLPSLFEIRY ETRUTGRTODELLFSNSTRLSFETKRISVFIGDTALLKFKQEVKFRIVTLFSDFRIY ETRUTGRTODELLFSNSTRLSFETKRISVFIGDTALLKFKQEVKFRIVTLFSDFRIY KTSLNILIKDFKSNLIQOSDLGVISKTTQLSSHPILGDMSIQVQVNDQTYVQS FQVSETVLPKEEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVPLTFLPLSFWGK KKNITKTFKINGSANFSFNDEMKNVNDSSNGLSEYLDLSSPGPVEILTTVTESVTGI SRNVSTNVFFKQHDYLIBFPDXEMKNVNDSSNGLSEYLDLSSPGPVEILTTVTESVTGI SRNVSTNYTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGS KSMANHSLFKSPSKTYIQLKTRADENIXVGSPFLVVSGNKELKELSYNVVSRQQLVA VGKONSTWFSLTPENAGWTFKACVIVYYIEDDGIISDVLKIFVQULVFKNKIKLYWSK KSSMAVHSLFKSPSKTYIQLTDANLTKDYIDGVYNAASNDITMENVVHELKIKIKLYWSY KAEPSEKVSLAISVTQDESIVATOVYNDASINSTMEGHTVDIHDFSLGS SPHVRKHFPETWIMLDTNMGSRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPV ELQAFQPFFIFUNLFYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDLGGLGLTTTPV ELQAFQPFFIFUNLFYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDLGCHUTUKAEGI INATGHQQTLLVPSEDGATVLFFIRFTHLGEIPITVTALSFMRQGYQRELLYQREDG SFSAFGNYDESGSTWLSAFVLRCFLEADPYIDDLKEKALSFMRQGYGRELLYQREDG SFSAFGNYDESGSTWLSAFVLRCFLEADPYIDDLKEKALSFMRGGYGRELLYQREDG SFSAFGNYDESGSTWLSAFVLRCFLEADPYIDDLKEKALSFMRGGYGRELLYQREDG SFSAFGNYDESGSTWLSAFVLRCFLEADPYIDDLKEKALSFMRGGYGRELLYQREDG SFSAFGNYDESGSTWLSAFVLRCFLEADPYIDDLKEKALSFMRGGYGRENGEFWDP GRVHHSELQGGNKSPYTLTAXIVTSLLGYRKYQVFRI" 676 c 731 g 1021 t	/organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606" 1133316 /note="unnamed protein product" /codon_start=1	neria Suthe acid 37069 (CA)	from Patent GI:25261494 (human)	
Length: Matches: Conservative: Mismatches: Indels:	SO 1236 . IT SO 12	sapiens" nic DNA" :9606" protein produc	257 ,,,	3535 bp DNA WOO2070696.	
3535 1061 1 0	CTAALAVAPGPREJ LEAGGVFEKGSFF, FIQTDKALYKPKQJ SKTFQLSSHPILGJ SHTTAKYTYGKPVJ SHITTAKYTYGKPVJ SHITTAKYTKYTRADV UPQSGTFKIEFPIJ SSPPELVVSGNKRI UPQSGISWATASIDITME VPDASITSWATGI IVPDSITSWATGI	(T	Catarrhini; Hominidae;) catarrhini; Hominidae;) polypeptides and methods EP-2002; d, Robert D. (CA)	linear	
	LVTAPGI IRPGAN TLTLESEPINSADS EVKERI VTLESEPI DWS 10 VQVNDQTYY KGDVTLTFLPLSEPI GYVELLTLTELPLSEPI ROGLTLEERRANNV LEDSSELQLKAYFI LKELSYMVVSRGQI VQLVFKNKI KLYM NVVLELLYNTGYY FVI SEDLGLGLTTT FVI SEDLGLGLTTT I EKKSDKFD ILMTS FVI SEDLGLGLTTT I IKKSDKFD ILMTS ASDAVTQMI LVKAI ASGAVTQMI LVKAI ASGAVTA ASGAVTANI		; Homo.	PAT 22-NOV-2002	
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21 73 41	201 LeuGlYASpTrpSe	ωμω	121 Algueuser		95- 1 1 21 21 33 41 61 93
ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 	LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln		A GLEUSELTHESILTHEN SAAIGTIESE VALHETIEGINITH SEDYBALALEUTY	GlulysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu	Gaps: 4 (1-1428) x AX534944 (1-3535) MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu
ThrGluSerVali GACAGAATCAGTTI	pTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSe		FINESTITITE YBATGITESET VALFRETTEST THAN THE FINESTITES TO THE STRIPT HE STR		Gaps: x AX534944 (1-3535) x AX54494 (1-3535) x AX5449
TG USerValThrGlyIleSerArgAsnValSe AGAATCAGTTACAGGTATTTCAAGAAATGTAAG PTyrIleIleGluPhePheAspTyrThrThrVa	SINASPGINTHETYETYTGI			SerLeuProLeuA	O LeuLeuCysvalc
rgAsnValSerThr GAAATGTAAGCACT YrThrThrValLeu	YrGlnSerPheGln	TCCAACAGTGGTT erSerHisProIl	SpPheLysProTy	snSerAlaAspGI	ysThralaalale
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Aichi 466-8550, Japan
Location/Qualifiers
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Submitted (11-MAR-2002) Department of Pathology, Nagoya University
Only of Medicine. 65 Tsurumai-cho, Showa-ku, Nagoya,
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SerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePhe
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693 ThrTrpleTrpLeuAspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThr 712 	673 ValasplleHisAspPheSerLeuGlySerSerProHisValargLysHisPheProGlu 692	GlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHisIle 67	PheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIleAsp 652 	GluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaVal 632	AspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHis 612 		LeuValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGlu 	ValTyrTyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln	AsnSerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysVallle 53	3 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLysGln ::: 5 TTCAAGGACTTAAGCTATATGGTAATATCAAAGGGACAGTTGGTGGCTGCAGGCAAACAA			ProfleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSer	413 GluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPhe 432 ::: :: ::: :::	395 GlnArgAgnTyrThrGluTyrTrpSerGlySerAgnSerGlyAgnGlnLygMet 412 	375 AlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIleThrValThr 394 :::	1360 TCAAGAATGCAAGCACCAATGTGTTTTTCAAGCAACATGATTACATCATTGAGATTTT 1419 355 AspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArg 374	
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1053 VALITIKSETLEGULEGUTYTYKATGLYBITYTGINFTCHABILLERBYWALGITGIUSELLE 10/2 ::: 3505 GTGACTTCTGTCCTGGGATACAAAAAGTATCAGCCTAATATCGATGTACAAGACTCAATC 3564	ValizeH.8SerGluLeUGLNGLYGLYABDLY8SERFROWALIDTLEWLDTALATYFILE	3 ThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArg	993 LeuArgCysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArg 1012 	973 SerPheSerAlaPheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheVal 992 	953 AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGly 972 	933 IleTyrIleLeuAspTyrLeuThrLysLysGlnLeuThrAspAsnLeuLysGluLys 952	913 SerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsn 932 	GluargValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsmGlyLeuAla 	873 LeuGlnSerThrLeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySer 892 :::::: :::::: ::::::	853 AlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArg 872 :: ::		GluaspGlyAlaThrValLeubheProIleArgProThrHisLeuGlyGluIleProIle :::::		773 TyrleulyskspalathrGluVallysVallleIleGluLysSerkspLysPheAspIle 792	ASTLEUPTOTYTSETVALITEATGGIYGIUGIUFRATABLEUGIUITIETINTITEPREASH 	s Leugly-Leuthrinztnitztovaligituleuginalarheginitztorherneileeneugin 	valProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly	

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PheCysPheLysLeuLeuTyrPheMetGlu 1425
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Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkine, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Millahy, S.J., Bonak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: bento-soares@uiowa.edu, tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-MAY-2003) National Institutes of Health, Mammalian Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: Plate: Row: Column: 0.
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas L. Casavant.
Web site: http://genome.uiowa.edu
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Proc. Natl. Acad. Sci. U.S.A. 9
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/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MGC:63463 IMAGE:6406841"
/tissue_type="Brain, enriched mouse brain, in the content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                      IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
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VNNVHRKNINFESQRT I KILDFYSV I RGEEPALEVS I TNYLKDTI KVVI I EEGDSFDI LWTS
NDTNGTI YRKTVQVFRDNGKTI LYFILDFLOSS DEDLMYSS I TSWVASAFVI SEDSFEJ ILWTS
NDTNGTI YRKTVQVFRDNGKTI LYFILDFLTKKYQDNU LEESDSFDI LWTS
SILRMFYGCGEQOMNI YFAPNI YILDSLTKKKYQDNI DVDLHRTYTWLNAKKFNGEFW
EPGRV I HSELQGGTKS PVTLTAY I VTSVLGYKKYQDNI DVDS I KFLEFEESRG I SDN
YTLAI I SYALSTWGSFKAEEALMLLMQRSEKEGOTQFMLSSGPALGSGFALCQLKWDY
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LYSVOMDYKERRAAVRTAGVKLSSCYLSSCYLSPDTNCKSHTDGATDSLRRSSSLLVFCCSVL
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                                                     ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsnLysArg
                                                                                                                           SerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr 472
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1213 SerSerPro	GluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyPro 1 ::: ::::	1173 ASINGETLEUGLYGLYPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSer 1192 	PheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeuSerArgGlnArg 1	AspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAlaLeuLeuSerHis	TrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeuSer	ThrTyrAlaLeuSerSerVal0lySerProLysAlaLysGluAlaLeuAsnMetLeuThr ::: ::: ::: TCCTATGCCCTGTCCACAGTCGGGAGCCCTAAAGCAGAGGAGGCTTTGAACTTGCTGATG	1073 H18PRELEUGIUSETGIUPRESETARGGIVILESETARGARTYTINTLEUAIALEUITE 1092	ValThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAsgValGlnGluSerIle	ValileH:sSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlafyrile	ThrTyrThrTrpLeuLy8GlyHisGlnLysSerAsmGlyGluPheTrpAspProGlyArg	LeuArgCysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArg	SerPheSerAlaPheGyAshTyrAspProSerGlySerThrTrpLeuSerAlaPheVal 	AlaleuserPheWetArgGlnGlyTyrGlnArgGluLeuIeuTyrGlnArgGluAspGly :::	1 1 1 1 1 1 1 1 1 1	SelfeulleAigectrolyne, ycyselychusinasmetleasminealarioasm 	GUMATGVELGINIALIENTALIEGIYASDVALIEUGIYAFOSETILEASRGIYAEUALI 	LeuginserinrieulyeinrieuserbeserbeProProAenThyValThrclySer ::::: ::::

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                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     This clone (DKFZp762L1111) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                               Homo sapiens mRNA; cDNA
AL834478
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Location/Qualifiers
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organism="Homo sapiens"/
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                                      GluThrTrpIleTrpLeuAspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluVal
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GAGACTTGGATTTGGCTAGACACCAACATGGGTTCCAGGATTTACCAAGAATTTGAAGTA
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/ protein="id="CAD39137.1"
/ protein="id="CAD39137.1"
/ db_xref="gi:21740253"
/ db_xref="gi:21740253"
/ translation="hypothetical protein"
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/clone_Tib="762 (synonym: hmel2). Vector pSport1; host
DH10B; sites NotI + SalI"
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/db_xref="taxon:9606"
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Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Wishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
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Homo sapiens cDNA FLJ38569 fis,
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FQVSETVLPKFEVTLQTFLYCSNNSKHLNGTITAKTYTGKPYKGDVTLTFLPLSFWK
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SRNVSTNVFFKQHDYIIEFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVIT
VTQRNYTEYWSGSNSGNOKMEAVQKINTVPQSGTFKLEFDLEDSSELQLKAYFLGS
VTQRNYTEYWSGSNSGNOKMEAVQKINTVPQSGTFKLEFDLEDSSELQLKAYFLGS
KSSMAVHSLFKASPSKTYLQLKTREDBULKYGS PEELVVSGKRRLKELSYMVUSRGQLVA
VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKV
KAEPSEKVSLRISVTQDDSIVGLVANDKSVNLMNASNDITMENVVHELELXMTGYYLG
VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIIGDVLKIPVQLVFKNKIKLYWSKV
KAEPSEKVSLRISVTQDDSIVGLVANDKSVNLMNASNDITMENVVHELELXMTGYYLG
MFMNSFAVFGEGCLWMLTDANLTKDYIDGVYDNLFGTQEAL"

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/db_xref="G1:21755237"
/db_xref="G1:21755237"
/translation="MOSPPLITAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI
/translation="MOSPPLITASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY
GVELLEHCPSQVTVKAELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY
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/clone_lib="HCHON2"
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                                           ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
                                                                                             ThriysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys
                                                                                                                                                                                                                                                                           LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle
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Unc-5 constructs and screening methods
Patent: WO 0073328-A 68 07-DEC-2000;
Devgen NV (BE)
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                        LysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSerLysHisLeuAsn
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           AAATTTGAAGTGAATATCAAGACGTCTTCGTTTATAACTATTAACGAT---GATTTGTCA
                                                                                                                                                                          LysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAspLeuGlyValIleSerLys
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                                                                         -----ValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrValLeuPro
                                                                                                            GAGCTCCAACTTGCCGAAGAGACTCTCCTTGGAGATTGGTTTATCGAGGTGGAAACCTCG
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Db 2794 CTCAACAATAACTCTTCGGATTTCTCCAAAAATCTTGAGCTTATCTGGCCAAACGAC 2850 Oy 888 ThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeuGlyProSer 907	. 2674 848 2734	811 ProSerGluAspGlyAlaThr	AGGAGCAAGATGTAACAGTGACGAGGTTGGCCAACAAATGTTCGTATTGTG	2374 GCTCCAACGACTTCAAAACTTCGCGTGTTTCGTCCATTTTTTATTCAACTCAATCTTCCA 756 TyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLys			610 GENERAL VALLES AND THE PRINCIPLE OF	1816 A 593 A 1873 G 613 G 1933 G 627 - 1993 G

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                                                                            GATATCAACATAAGAAACGCAATTGTTCTCCAATCCTATCAACTATCTTCATTGAATGAT
                                                                                                                                                     AlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMet 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValSerSerGlu-----SerLysLeuSerAspSer-----TrpGlnProArg 1138
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
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                                             GTGTCAACAACCGCGGCGCCAGTTAAACCAGCC---ACTTATATGCTTGTCGCCCCAGCA 138
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                                                                          ValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThrAlaProGly 34
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330 ServalThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyr 349 :::	290 AlaAsnPheSerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeu 309	GlyThr1leThrAlaLysTyrThrTyrGlyLysProValLysGlyAspValThrLeuThr::::	192 INTERIGIAL CUSTSETH SPROILE LEUGLY ASPIT POST LEGINVALGIN 209 193 INTERIOR CONTROL OF THE PROILE LEUGLY ASPIT POST LEGINVALGIN 209 616 GAGCTCCAACTTGCCGAAGAGACTCTCCTTGGAGATTGGTTTATCGAGGTGGAAACCTCG 675 210ValabapgClnThrTyrTyrGlnSerPheGlnValSerGluTyrValLeuDro 227 211	TTCATCCAAACAGATCGAGCAATCTATCGGCCTGCTTCTCTTTGTTCGATACCGGCCAATT TTCATCCAAACAGATCGAGCAATCTATCGGCCTGCTTCTCTTTGTTCGATACCGGCCAATT ThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeuIleLysAspPro	139 GTAGTGCGACCCGATCAACCCTTCTCCGTTTTGCATGAACCTTCTGAAACCAAGCTACCGAT 198 55 GInValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeu 74 :::::::::::::::::::::::::::::::::::
N N N	Qy 627Met 627 Db 1993 GAGGCAATTGATAGAAAGAAGAGGTCCATTTGGAGACCTTGGTGGGGAATTGGAGGGAG	Db 1816 AATGTGAAGTTTAAGGTCACATCTGACAAGAACTCTTTGTTGGCCTTCTTGTGGGTA 1872 Qy 593 AspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHis 612 [Db 1459 GCCGTGAGCCCAACGAAGAGTTTCCTGCAGCTTTTGGCTGAFAATGAGGAGCTGTTGAT 1518 Qy 479 ValGlySerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyr 498	388 AsnValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSer

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1369 GluProArgArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAsp	VQ	
1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368	QY db	1017 LeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallleHisSer 1036
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1314 IleSerLeuSerGluThrValLy8Ly8ValGluTyrAspHisGly 1328 ::: :::::::	p, 8	
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1254 ArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsn 1273	Qy Db	917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936
1234 GlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArg 1253	Qy dd	897 IleThrAlaileGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916 ::: :::::: 2911 TTAGATGTGATTGGTGATATGATGGGACCACTGTTAAACAATGCTCATAAGCTCGTACAA 2970
1221 ValGlnProMet	Qy dd	877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896
ThrValThrGlyProSerSerProSer	\$ &	857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876 ::: ::::::::::::::::::: :::: 2794 AAAGTAGAATATTCCATTTGTCATTGACCTCAACAATAACTCTTCGGATTTCTCC 2853
LeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnVal	o b oy	837 LeuSerProThrAlaSerAspAlaValThrGlnMetIleLeuValLy8AlaGluGlyIle 856 ::::::
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AlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrp ::: ::: GCAGTTCTTTCTTACCTCGCCCAAAATCAAACCTCAGAATCTCTCTC	Db Qy	800 AsnAlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThr 817
1132 SerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyr 1147	Оу	785GluLysSerAspLysPheAspIleLeuMetThrSerGerGluIle 799 ::: ::: ::: 2554 AAGTATGATAAAGACTCTGGGTTACGATCTCCTGAAGAAAGA
1115AlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeu 1131	Ωу	765 AlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIle 784
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GluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAla) B Q	725 PheVallieSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGluLeuGlnAla 744
	d Qy	705 IleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrCGly 724
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Db 4366 GATCCGGAGGAGCAGCTCAAAATGACATACGCCGCCAAGCAAAACACGATCGCTGCAAGAG 4425

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Search completed: January 17, 2004, 08:32:16

Job time: 11145 secs

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Pred. No. is the number of results predicted by score greater than or equal to the score of the No. chance to have a result being pri printed,

and is derived by analysis of the total score distribution.

Result No.

Result No.	No.	Score	Query Match 1	Length	BDB	ID	Description
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	41	1401	19.1	4487	24	ABK92035	DNA encoding novel
	42	1400	19.1	4615	23	AAS92193	encoding
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ALIGNMENTS

RESULT 1 AAD49434

AAD49434 standard; DNA; 4369 BP.

AAD49434;

TX SX FX EX EX PX AX B 24-MAR-2003 (first entry)

Human r150 gene #1.

Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.

Homo sapiens.

Key

Location/Qualifiers

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Alignment
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                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is a gene encoding human r150 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for
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                                                                                                                                       TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr
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821 ProlleArgProThrHisLeuGlyGluIleProlleThrValThrAlaLeuSerProThr 840 	AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe	LysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsn 	GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal	GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArg 	valalaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrThrProVal	MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp	GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn 	AlaGluArgPheMetGluGluAsmGluGlyHisIleValAspIleHisAspPheSerLeu	LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 660	TYrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 6	AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	InLeuvalPheLysAsnLysIleLys 560 	521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540	501 ValSerArgGlyGlnLeuValAlaValGlyLyeGlnAsnSerThrMetPheSerLeuThr 520	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500
Qy 1181 ThrGlnAspThrThrValAlAleuLysalaleuSerGluPheAlaAlaleuMetAsnThr 1200		Qy 1141 AspIleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu 1160 	Oy 1121 MetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeu 1140	Qy 1101 SerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGly 1120	Qy 1081 ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGly 1100	Qy 1061 LysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer 1080	Qy 1041 GlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1060 	Oy 1021 GlnLysSerAsnGlyGlubheTrpAspProGlyArgVallleHisSerGluLeuGlnGly 1040	Qy 1001 ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis 1020 	Qy 981 AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1000	Qy 961 TyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyr 980	Qy 941 LysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGly 960	Qy 921 CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr 940	Qy 901 GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 920	Qy 881 SerPheSerPheProProAgnThrValThrGlySerGluArgValGlnIleThrAlaIle 900		Qy 841 AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr 860

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/product= "Gova"
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2002-713460/77.
DB; AAO19372.
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New isolated oligonucleotide binding to having a single nucleotide polymorphism and/or Govb allele, useful for treating a region of CD109 nucleic acid that distinguishes a Gova blood disorders e.g. alloimmune

Claim 6; Page 23-29; 69pp; English.

The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelets refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova coding sequence.

BP; 1296 A; 837 Ç 922 G; 1280 T; 0 other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:

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US-10-020-095-4 (1-1428) x AAL49815 (1-4335)
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                         ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
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GLIAGE GCTGAG	D Q D Q	ASDValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320
TATTAT LeuThr TTGACA	}	LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsmIle 280
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1501 GTATCCAGGGGACAGTTGGGTGGCTGTAGGAAAAGTTCAACAAGTTCTCTTTAACA	ត្ត	LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160

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                                                     GluArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro-----
                                                                                   ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr 1200
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 CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGGTACAGCCA
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CD109; alpha2 macroglobulin; thioester; cerebroprotective; c immunosuppressive; haemostatic; anticoagulant; thrombolytic; cardiovascular; vasotropic; gene therapy; CD109 K1; gene; ss
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated nucleic acid molecules encoding CD109 CD polypeptides. These nucleic acid molecules include the human cDNA CS sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its minmetic, or the anti-CD109 antibody is useful CC contracting or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of 1 lymphocytes and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC citivation, increased or impaired platelet aggregation and CC citivation, increased or impaired activation of the coagulation and CC citivation, thrombosis, embolism, peripheral vascular disease, cc thrombocytopenia, thrombocythemia, autoimmune diseases, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human CC CD109 K1 CDNA sequence.
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                                                                                                                                                                ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu
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Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence. Note: This sequence is stated to encode human CD109 protein shown in figure 17 of the specification, but this does not appear to be the case. Disclosure; Fig 17; 127pp; English.

Sequence 5882 BP; 1696 A; 1173 C; 1241 G; 1772 T; 0 other;

Alignment

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                  LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr
                                                                                            ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
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    AAGCCAAAGCAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC
                                                 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
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LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu

SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	euPhe 460 GTTT 1492 1552	ThrvalproglnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440 ThrvalproglnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440 ThrvalproglnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440 Db	360 1192 380 1252	ASSIVALMETAS DE SER SER ASSIGLY LEUS ER GLUTY LEUAS DE LA SER SER PROGLY PRO 320	AAATATT 952 AAATATT 952 AAATATT 952 AATGAAA 1012	0 N 00 N	ADARCCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAAT
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TyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla
                            ATGGCAGTTAATATTTCCGCAAATGGTTTTTGGATTTTGCTATTTTGTCAGCTCAATGTTGTA
                                                                                         CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioseter-containing proteins. The CD109 polypeptides can be compressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation. These CC are also useful for treating cardiovascular disorders, stroke, myocardial confirmation, thrombosis, embolism, peripheral vascular disease, creaming these conditions. The present sequence represents the human CC treating these conditions. The present sequence represents the human CC chica the conditions. The present sequence represents the human cconditions.
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The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inosicol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein encoding DNA.
                                                                                                                                                                                                                                                                            Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer -
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14-FEB-2002; 2002US-356163P.
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P-PSDB; AAE32013.
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Sequence 5883 B₽; 1696 Α, 1173 Ç 1241 G; 1772 T; 1 other;

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Query Match:
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LysThrSerLeuAsn11eLeu11eLysAspProLysSerAsnLeu11eGlnGlnTrpLeu
                                                                                                                                       IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
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521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540 	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520 	481 SerProPheGluLeuValValSerGlyAsmLysArgLeuLysGluLeuSerTyrMetVal 500 	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480 	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460 	ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu .	TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 4	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400 	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380 	341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360 	321 ValGluileLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340 	301 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300 	261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnTle 280 	241 MetABnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260 	221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240 	201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220 	181 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIle 200 	93
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                                                                        CTGATTGACACACACAACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGGTACAGCCA
                                                                                                                      GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTT 3772
                                                                                                                                                                                  ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr
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Human; platelet alloantigen; Gova; Govb; single nucleotide polymorphism; SNP; biallelic; bleeding disorder; post-transfusion purpura; post-transfusion platelet refractoriness; haemostatic; vaccine; neonatal alloimmune thrombocytopenia; gene; ss.
                                                                                                                                                                                                                                                                                                  Human platelet alloantigen Govb coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a sequence capable off binding specifically to a CDIO9 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion plattelet refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Govb coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune
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P-PSDB; ABB82166.
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New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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Claim 1; Fig 1b; 156pp; English.

CC The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC transplantation, or bone marow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human CC CD109 KI variant CDNA sequence.

Sequence 4761 1419 A; 913 ç 1016 G; 1413 T; 0 other;

Best Local Si Query Match: DB: 밁 Ś 문 Ś 밁 Ś 밁 8 밁 Ś 밁 Ś 밁 á US-10-020-095-4 (1-1428) x ABQ79965 (1-4761) Percent Similarity: 473 121 413 101 353 293 233 173 113 81 61 41 Similarity: 21 ш ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA ATGCAGGGCCACCGCTCACCGCCGCCCACCTCCTCTGCGTGCACCGCCGCGCGCTG GAGCTGCTCAAGACAGCATCAAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGGTCTTT 0 7317.50 98.75% 98.69% 99.58% 24 Gaps: Length: Matches: Conservative: Mismatches: Indels:

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LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr

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AAGCCAAAGCAAGAAGTTTCGCATTGTTACACTCTTCAGATTTTAAGCCTTAC

rccaggggacagtiggtggctgtaggaaacaaaattcaacaatgtict	01 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 5	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480 	1 LeuGlnLeuLyBAlaTyrPheLeuGlySerLyBSerSerMetAlaValHiBSerLeuPhe 4	ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu	TYrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 4	ThrLeuglugluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 4	1 LysproSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 	ASDVAlPhePheLySGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 3	valGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 3 	AsnValmetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 3	81 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspG 	61 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysLysAsnIle 28	1 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 26	rGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTy 	01 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 22 	81 SerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIle 20 	161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180
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MetAlaValAsnTleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValVal
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CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 KI-H7; variant; gene;
                                                                                                                                                                                                                                                                                                  Human CD109 K1-H7 variant protein encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1. CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful for treating or detecting a disease or disorder, e.g. conditions
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     TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA
                       SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal
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                                                                                                                                         CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT
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1218LeuAlaValValGlnPro 1223	1201 GluArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro 1217	3653 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTTGCAGCCCTAATGAATACA 3712	Threlaberthettellalerous and server and the company of the company	J H⊦	MCCUINFREITPYALSERSERGIUSERLYSLEUSERABSSERITPGINFROARGSERLEU 	SerProLysAlaLysGluAlaLeuAsnMetLeurhtTrpArgAlaGluGlnGluGlyGly	ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGly	Lyst AAGT	1041 GlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1060 	021 GlnLysSerAsnGlyGlubheTrpAspProGlyArgValIleHisSerGluLeuGlnGly	ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis	AspProSerGlySerThrTpLeuSerA.aPheValLeuArgCysPheLeuGluAlaAsp 	TyrGlnArgGluLeuLeuTyrGlnArgGluAepGlySerPheSerAlabheGlyAenTyr	941 LyslysLysClnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgClnGly 960 	CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr 	GLYASDVALLEUGLYPTOSETLEASNIGLYLEUALGSETLEULLEATGMETPTOTYTGLY	Serreserreprocassint valuar by serguary algunt leinfalaile	93 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, insue growth activity, activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, activity activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
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Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
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GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe
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GlyGlucluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal 	QY dd	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420 	J ,
741 GluLeuGlmAlabheGlmProPhePheIlePheLeuAsmLeuProTyrSerVall1eArg 760	Qy Db	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400 	· \
ValAlaThxGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal	DЬ	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380 	•
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41 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspClyValTyrAspAspAla 	Ωy	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300 	٠ <i>٦</i>
TYTTYTLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal	D Qy	261 Ly8GlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLy8Ly8Ly8Ly8AsnIle 280 	U ~
	Qy dd	241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260 	•
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27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                       Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
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                                     LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly
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SerProLy881aLy8G1uAlaLeuAsmMetLeuThTTpArgAlaG1uGLnG1uGLYG1y 	υb	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArg 760
ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGly	ОУ	721 ValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal 740
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                                                                                                                                                                                                              cell surface antigen,
                                                                                                                                                                                                                                          (first entry)
/*tag= a
/product= "Human CD109 protein"
/product= "Funch (pos:2044..2046, aa:Xaa)
/note= "Xaa corresponds to Ser, Tyr; No start
and stop codon"
/partial
                                                                                                  Location/Qualifiers
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Pred.
               Alignment
                                                                        The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence.
                                                                                                                                                                                                                                                                                               Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
No.:
                                                Sequence 4146 BP;
                                                                                                                                                                                                                                                  Claim 7; Page 109-112; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Philip
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14-FEB-2002; 2002US-356163P.
                                                                                                                                                                                                                                                                                   treating cancer
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                                              1260 A;
                                              776 C;
                                              885 G; 1224 T; 1 other;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: Score: 0 7081.00 99.86% 99.78% 96.37% 25 Length:
Matches:
Conservative:
Mismatches:
Indels: 4146 1379 1 2 0

US-10-020-095-4 (1-1428) x AAD49436 (1-4146)

Gaps:

CCTAGIAAGACAIACAICCAACIAAAAACAAGAGAIGHAAAITAIAAAGGIGGGAICG 138 PheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetValVal 501 [CCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGAGGATTC LeuLygalaTyrPheLeuGlySerLysSerSermetalaValhisSe	21 140 21 200	PheLysGlnHisAspTyrlleIleGluPhePheAspTyrThrThrValLeuLys 3	41	VARICALLIAMA GOLACCAL CACGCCAMOGLA IACALA GOGA VARITAT LOUTH PheLeu ProLeu Ser PheTrpGly Lys Lys Lys Lys Lys Lys Lys Lys Lys Ly	UTYTVALLEUPTOLYSPHEGIUVALThrLeuGInThrProLeuTyrCysSerMet 2	0 1 8 8 1 2 1 4 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
842 SerAspAlaValThrGlnMetileLeuValLysAlaGluGlyIleGluLysSerTyrSer 861	802 ThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhePro 821	CTCCAAGCCTTCCAACCATTTTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGAGGT Z GluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLys	702 GlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSerTrpVal 721	662 GluArgPheMetGluGluAsnGluGlyHiBIleValAspIleHiSAspPheSerLeuGly 681	622 TyrLeuGlyMetPheMetAbnSerPheAlaValPheGlnGluCygGlyLeuTrpValLeu 641	582 GInDroaspSerilevalGlyIlevalAlavalAspLysSerValAsnLeuMetAsnAla 601	1501 GANAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTAATATTGAAGATGATGGGGAA 1560 542	522 GluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGlyGlu 541

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ValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGln
                                                           CAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTGGAT
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    WPI; 2003-093100/08
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14-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein
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    CAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAATGCC
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                                                                      TyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThr
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1305 SerGlyPheMetValProSerGluAlaIleSerLeuSerGluThrValLysLysValGlu 1324	1285 CysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeu 1304 	1265 AspLeuAspVəlAlaVəlLysGluAsnLysAspAspLeuAsnHisValAspLeuAsnVal 1284 	1245 AsnValLysAlaSerGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPhe 1264 	1225 AlaValAsnīleSerĀlaĀsnGlyPheGlyPheĀlaīleCysGlnLeuAsnValValTyr 1244 	1218	1202 ArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro 1217 	1182 GlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGlu 1201 	1162 IleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThr 1181 	1142 IleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGly 1161 	1122 GlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAsp 1141 	1102 ProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMet 1121 	1082 GlylleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer 1101 	1062 TyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSerArg 1081 	1042 ASnLysSerProvalThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061 	1022 LysSerAsnGlyGluPheTrpAspProGlyArgVall1eHisSerGluLeuGlnGlyGly 1041 	1002 TyrileAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGln 1021 	982 ProSerGlySerThrTrpLeuSerAlaDheValLeuArgCysPheLeuGluAlaAspPro 1001 	962 GlnargGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAsp 981

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                                         The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1. CD109 K1.-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 can be carparented by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                      New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal
                                                                                                          LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln
                                                                                                                                                                 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIle
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                                              ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer
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The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful for treating or detecting a disease or disorder, e.g. conditions
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                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4b; 156pp; English.
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                                                                             associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired activation of the coagulation and/or fibrinolytic systems, or impaired activation of the coagulation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human
  Sequence 3535
                                                        K15 variant cDNA sequence.
BP; 1107 A; 676
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Query Match: DB:

Percent Similarity: Best Local Similarity:

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Conservative: Mismatches: Indels:

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652		b 593	뮍
180	LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu	у 161	S
592		b 533	닭
160	LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr :	y 141	ð
532		b 473	닭
140	ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr	у 121	ð
472		b 413	닭
120	IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr	y 101	ঠ
412		b 353	뮹
100	GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu	у 81	ð
352		b 293	문
80	GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe	у 61	ð
292		b 233	닭
60	AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla	y 41	Ş
232	GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGCCCCGGAGGA	b . 173	문
40	AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40	у 21	S
172	ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG	b 113	밁
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ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA

GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT

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541 GluII eileSerAspValleuLygII eProValchicelValPheLysAsnLygII eLys 560	TCGCCTTTTGAGGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATG ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeu	GlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValH	TYTTEPSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420	GTTCTTCAAGCAACATGATTACATCATTGAGTTTTTGATTATACTAC	TAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	AAAGGAGACGTAACCGCTTACATTTTTACCTTTATCCTTTTGGGGAAAAAAAA	snSe
GAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCAGATGCCTTATGGC 2813 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTTCATTGATTCAGATGCCTTATGGC 921 CysGlyGluGlnAsnMetileAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr	Qy 861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 880	Oy 801 AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe 820	8=8 검=8	721 ValalaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrTrvVall	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn	641 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr	Qy 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620

g	2993	2993 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT 3052
ş	981	AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1000
8	3053	GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3112
Ş	1001	ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis 1020
9	3113	3113 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3172
Ş	1021	GlnLysSerAsnGlyGluPheTrpAspProGlyArgVallleHisSerGluLeuGlnGly 1040
D _D	3173	3173 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3232
Ş	1041	1041 GlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1060
문	3233	GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCGGGATATAGA 3292
Ş	1061	1061 LysTyrGln 1063
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Search completed: January 17, 2004, 01:15:04 Job time : 983 secs

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Result
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-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                US-09-241-606-1

US-09-016-434-1174

US-08-447-411-1

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US-08-793-126-2

US-09-132-271-2

US-09-142-334-23

US-09-142-334-23

US-08-662-227-1

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Sequence 322, App Sequence 256, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	e 83, Ape 257, Ape 255, Ape 255, Ape 20, App e 11, App e 11, App e 18, App e 1, App	102	Sequence 1, Appli Sequence 3, Appli Sequence 56, Appli	71010 1000 1

ALIGNMENTS

RESULT 1 US-09-241-606-1

Sequence 1, Application US/09241606 Patent No. 6472140

GENERAL INFORMATION:

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Alignment
Pred. No.:
                 Percent Similarity:
Best Local Similarity:
                                                                                                                     US-09-241-606-1
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovace, Dora
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                            FEATURE:
NAME/KEY: sig_peptide
LOCATION: (44)..(112)
                                                                                                                                 NAME/KEY: mat_peptide
LOCATION: (113) ... (4468)
                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (44)..(4468)
                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                    Scores:
                                                                                                                                                                                                                                                                                                                         4577
1.49e-142
1441.00
46.20%
29.06%
19.61%
 Conservative: Mismatches: Indels:
                                                  Length:
Matches:
4577
451
266
551
284
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. <i>8</i>	gb Qy	D Qy	B 8	DD QY	용 왕	B 8	B 8	용 성	B 8	유 성	B &	g 4	B 8	용 성	문 왕	B 8	B 8	DB:
317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316 989 TATGAAATGAAA	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	272SerPheTrpGlyLys 276 ::: ::: ::: ::: ::: :::	264 ValThrLeuThrPheLeuProLeu	244 LY8HisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysBroValLysGlyAsp 263 ::: ::: ::::::	224 TyrValleuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223	186 LeuGlyVallleSerLy8ThrPheGlnLeuSerSerHi8ProIleLeuGlyAspTrpSer 205	167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166 ::: :::::: 476 AAATTTCGTGTTGTCTCCATGGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA 535	127 LysArgileSerValPheileGlnThrAspLysAlaLeuTyrLysBroLysGlnGluVal 146 ::: :::	107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	90 LeuProSerLeuProLeuAsgSerAlaAsgGluIleTyrGluLeuArgVal 106 :::::: :::: ::::: 311GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 364	72SerValLeuGluAlaGluGlyValPheGluLySGlySerPheLy8ThrLeuThr 89 ::: 263 TTCACTGACCTGGAGGCGGAGAATGACGTACTCCACTGTGTCGCCTTC 310	52 CysProSerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrVal 71	32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31	DB: Gaps: 59 US-10-020-095-4 (1-1428) x US-09-241-606-1 (1-4577)
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Db Oy	8 8 8	, B &	B &	g &	8 8	B 8	B 8	₽ %	g &	g 9	g Q	g Q	Db Qy	B &	B 성	B 6	В
2945 ATGCCCTATGCTGTGGAGAGCAGAATATGGTCCTCTTTTGCTCCTAACATCTATGTACTG 3004 937 ASpTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956	rALAILEG : ::: \GTTTTGG \TYrG1YC		857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876	842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856	833 ThrValThrAlaLeuSer	813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832	798 GluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	778 ThrGluValLysVallIeIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777	738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737	698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697 :::	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	652 ASpGlyValTyrAspAsnAlaGlu	632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651	1988 TATATTAATGGAATCACATATACTCCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2047
p Q	Q Q Db	& 음 &	, B &	P &	D Q	B &	5 B &	\$ \$ \$	·	B &	}	, B &	?	\$ B &	S B 7	S B 8	₹
GlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLysAsp :::	3956 TTGCCAGAGCTGCCTGGGGAATACAGCATGAAAGTGACAGGAGAAGGATGTGTCTACCTC 4015 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258	1216 SerProLeuAlaValValGIn	196 ALBLEUMECASNINGGINAZGINAZSINI LEGINVALITANGI VEPCOSETSETPRO	779		GAGATGACATCCTATGTGCTCCTC	**************************************	106 Leumsmetcheufnfifpargalagluginglugiyelymetginfhefip [U89 LEUALALEULIEIRTIYAA.ALEUSERSETVAIGLYSETPYOLYSA.ALYSGJUALA :: 482 AAAGCACTGCTGGCCTATGCTTTTGCCCTGGCAGGTAACCAGAGAAGGAAG	425	Seriemieugiyiyrargiyeiyrdir ::: gcccrrcrggagarrccrcrcacagro	305	ATATGGCTCTCCCAGAGGCAGAAGGACAATGGCTGTTTCAGGAGCTCTCGGTCACTGCTC	1015 ThrTmT.eulveGluVHisGluVivsGerasmGluGluDheTmassEbroGluArgVallle 1034	TITGGGGAGCGATATGGCAGGAACCAGGGCAACACCTGGCTCACAGCCTTTGTTCTGAAG	THE CT AS THE STATE OF THE STAT	957 MetavadladivTvrclaarodivLevTvrclaarodivLevTvrclaarodivLevTvrclaarodivLevTvrclaarodivLevTvrclaarodivLevTvrc

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Alignment Scores:
                                     ; LIBRARY: GENBA
; CLONE: g177869
US-09-016-434-1174
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US-09-016-434-1174
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                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                             TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                 NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: HEREWI CLASSIFICATION:
                                                                                                                                 STRANDEDNESS:
                                                                                                                                                       LENGTH: 4079 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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Best Local Similarity:
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                     953
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                     GTAAAA--
                                                       LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp
                                                                                                                                                                                                               ValThrLeuThrPheLeuProLeu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAATGAGACAGTGACTGTAAGTGCTTCCTTGGAGTCTGTCAGGGGAAACAGGAGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCCCTCCCTGCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC
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                                                                                               CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA
                                                                                                                                                                         GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA
                                                                                                                                                                                                                                                                                                                                TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA 772
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GlnLeuAsnValValTyrAsnVal 1246
                                                                                                      TTGCCAGAGCTGCCTGGGGAATACAGCATGAAAGTGACAGGAGAAGGATGTGTCTACCTC 4015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195
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Query Match:
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US-08-447-411-1
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                                                                                                                                                                                                                                                                                                                                                               US-08-447-411-1
                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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Patent No. 5773243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FRITZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FKITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3,
NUMBER OF SEQUENCES: 81
CORRESDANTEDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 08/043, THING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: ui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5211 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                             21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly
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 GAAGAGCAAATTTTGGTGGAGGCCCATGGAGACAGTACTCCAAAATCGCTTGACATCTTT 179
                              AsnValThrIleGlyValGluLeuLeu---GluHisCysProSerGlnValThrValLys
                                                                                                                               1755 S. Jefferson Davis Highway, Suite
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                                                             -TCCCACGGGGCTCTCTATACCCTCATCACCCCTGCTGTTTTGCGAACAGACACA
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Matches:
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	2157 TGTTGTCACTACATCAAAGGGATCCGAGAGTGAAAACCAACGGGAGAGCGAGTTGTTTCTG 2216 674AsplieHisAspPheSerLeuGlySerSerProHisValArgLysHis 689
B	p Q p Q p Q
1068 ValGInGluSerfleHisPheLeuGluSerGluPheSerArgGly7leSerAspAsnffyr 1087 3480 TrichartArGGCCACACAGATTATTTCCTCANAAGTATGACAAA "CTGCANAAGGCCTTAC 3536 1088 ThrieuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107 1088 ThrieuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107 1189 ThrieuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107 1191	999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu 1017

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Alignment Scores: 4.44e-88 Length: 5056 Score: 931.00 Matches: 381 Percent Similarity: 40.88% Conservative: 287	LENGTH: 5056 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-08-793-126-2	TELEPHONE: (617) 526-6000 TELEPAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	NAME: Baker, Hollie L. REGISTRATION NUMBER: 31,321 REFERENCE/DOCKET NUMBER: 102286.377 TELECOMMUNICATION INFORMATION:	APPLICATION NUMBER: US/08/793,126 FILING DATE: 07-FEB-1997 CLASSIFICATION: 42 ATTORNEY/AGENT INFORMATION:	2 2 S 2 S	, <u>, , , ,</u>	ADDRESSEE: HALE AND DORR LLP STREET: 60 State Street CITY: Boston STATE: MA	Farries, C NVENTION: N SEQUENCES: ENCE ADDRESS	; Sequence 2, Application US/08793126 ; Patent No. 5849297 ; GENERAL INFORMATION:	RESULT 4 US-08-793-126-2	1420 LeuLeuTyrPheMetGluLeu	Qy 1410SerSerValllePheIlePheCysPheLys 1419	Db 4497 AACATTTGCCGATGTGCAGAAGAAACCTGTTCCTTGCTCAACCAGCAGAAAAAAGATTGAT 4556	1394 GlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHisHis	QY 1374 AlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspVal 1393 :::- ::: ::: ::: Db 4437 TGTACCAAGTTCTACCAGATAAAGAAACAGGTCTTCTCAATAAGATATGTCATGGT 4496	Qy 1354 ValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGln 1373	Qy 1335 AspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLys 1353	Qy 1320 ValLystysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeu 1334 :::
Db 893 AITTECCTGACTGAATCCCTCAAGCGCATTCCGATTGAGGATGGCTCGGGGGAGGTTGTG 952 Qy 280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299 ::::::::	257 GlyLysProValLysGlyAspValThrLeuThrPhe	Qy 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr 256	Qy 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrPro 236 ::	Qy 202 GlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSer 218	Qy 182 GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu 201	Qy 163 SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSer 181 :::::: ::::: ::: Db 533 ACGGTCATGGTCAACATTGAGAAACCCGGAAGGCATCCCGGTCAAGCAGGACTCCTTGTCT 592	Qy 143 LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162	Qy 123 SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142	Qy 103 GluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeu 122	Db 350 GGGCGCAACAAGTTCGTGACCGTGCAGGCCACCTTCGGGACCCAAGTGGTG 400	290 AACCACATGGGCAACGTTCACGATCCCAGCCAACAGGGAGTTCAAGTCAGAAAAG	Db 230 GACTTCCCAGGCAAAAAACTAGTGCTGTCCÁGTGAGAAGÁCTGTGCTGACCCCTGCCACC 289 Qy 64 LysThrAlaSerAspLeuTh;ValSerValLeuGluAlaGluGlyValPheGluLys 82	Qy 50 GluHis	Db 170 ACCATGGTGCTGGAGGCCCACGACGCGCAAGGGGATGTTCCAGTCACTGTTACTGTCCAC 229	113 GGGAGTCCCATGTACTCTATCATCACCCCCAACATCTTGCGGCTGGAGAGCGAGGAG	Db 65 ĠĠrĊĊĊAGCĊſĠĊſĠĊſĊĊſĠCſŢACTAACCCACCſŢCCCĊſĠĠĊſĊſŢG 112 Qy 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg	US-10-020-095-4 (1-1428) x US-08-793-126-2 (1-5056) Qy 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22	Best Local Similarity: 23.32% Mismatches: 609 Query Match: 12.67% Indels: 358 DB: 2 Gaps: 63

	610 ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 629 :::	590 ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn 609	ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle	PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu	GluileileSerAspValLeuLysileProValGlnLeuVal	TrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly :::	LyBGlnAsnSerThrMetPheSerLeuThrProGluAsnSer :::	LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly .::::::: :::: ::::::::: ::: ::: :: :: :: ::	473ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490	457 HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr 472	437 AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal 456 :::::: :::	417 LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu 436	397 AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln 416 :::	379GlnLeuThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArg 396 :::::: :::: 1199 GCCTACCGAGTCCCGTGGCAGTCCAGGGCGAGGACACTGTGCAGTCTCTAACCCAGGGA 1258	LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	340 ThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrVal 359 ::: ::	320 ProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSer 339	300 LyBASHVAIMELASPSErSerASHGIYLEUSERGIUTYRLEUASPLEUSERSERPROGIY 319 :::::: :::
Qy 895ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly 910	Db 2930GACATCCCACCTGCAGACCTCAGTGACCAAGTCCCGGACACCCGAGTCTGAGACC 2983	2876 GCTGTTCGCACCCTGGATCCAGAACGCCTGGGCCGTGAAGGA	Valinioilmet.teletvallybalaciosiy legituybse; ylocioil 	825 2756	Qy 805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824	Qy 786LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804 :::	Qy 767 GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu 785	Qy 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766	Qy 727 IleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPheGln 746	Qy 707 GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726	GAGGACTTGAAAGAGCCACCGAAAAATGGAATCTCTACGAAGCTCGAGGACTTGAAAGAGCCACCGAAAAATGGAATCTCTACGAAGCTC	681 GlySerSerProHieValArgLysHisPheProGluThrTrpIteTrp	677	667 GluAenGlu	Qy 652 AspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGlu 666 :: :: 2135 GACGGCATGCGGAGAACCCCATGAGGTTCTCGTGCCAGCGCCGGACCCGTTTCATCTCC 2194	Db 2075 ACGGAGAAGCGAATGGACAAAGTCGGCAAGTACCCCAAGGAGCTGCGCAAGTGCTGCGAG 2134	2015 CAGAGGGCAGAACTTCAGTGCCCGCAGCCAGCCGCCGGCCG	Db 1955 GCCGGTGTTCTCCGACGCAGGGCTGACCTTCACGAGCAGTGGCCAGCAGCAGACCGCC 2014 Oy 644 644

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1205 IleGlnValThrValThrGlyProSerSerProSerProLeu 1218 ::: :::::	1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185 ::: 3809 CGTTGGCTCAATGAACAGAGATACTACGGTGGTGGCTATGGCTCTACCCAGGCCACCTTC 3868 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsn 1204 ::: ::: :::::::::::::::::::::::::	3692 AAAGATAAGAACCGCTGGGAAGCACCTTGGTAAAAGCACTTTGACTTTGTGCCTCCGGTCGTG 3808 3752 TATGCCCTCTTGGCCCTACTGCAGCTAAAAGACTTTGACTTTGTGCCTCCCGTCGTG 3808	AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn	TyrGlnProAsnIleAspValGlnGluSerIleHis	1026 GluPheTrpAspProGlyArgVallleHisSerGluLeuGlnGlyGly 1041	TrpLeuSeralaBheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp ::: ::::::::::::::::::::::::	3104 ACGCCACGGTCATCGCCTTTGCGGCCTTTGCGGCTGTGAAACGGGCACCACGGCCACGGTCTGCGCTTTGCGGCTGTGATGAAACGGAGCAGTGGGAGAAGTTCGGC 3163 950 LysGluLysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966 3164 CTAGAGAAGCGGCAGGGGCCTTTGGAGCTCATCAAGAAGGGGTACACCCAGCAGCAGCTGGCC 3223 967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986 :::::::: :	AGAATTCTCCTGCAAGGACCCCAGTGGCCCAGATGACAGAGGATGCCGTCGACGGGAALeuAlaSerLeuIleArgMetProTyrGlyCysGlyCluGlnAsnMetIleAsnPhe
PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US/08/793,126 FILING DATE: 07-FEB-1997 ATTORNEY/AGENT INFORMATION: NAME: Baker, Hollie L. REGISTRATION NUMBER: 31,321	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/132,271 FILING DATE: CLISCIFICATION.	ADDRESSEE: HALE AND DORR LLP STREET: 60 State Street COUNTRY: Boston COUNTRY: United States of America TIP: 02109 COMPUTER RADABLE FORM.	US-09-132-271-2 ; Sequence 2, Application US/09132271 ; Patent No. 6221657 ; Patent No. 6221657 ; GENERAL INFORMATION: ; APPLICANT: Harrison, Richard Alexander ; APPLICANT: Farriss, Charles Timothy ; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS ; NUMBER OF SEQUENCES: 2	4507 GGAAAGCTGTACCCGGTTCTACCATCCGGAAAAGGAGGATGGAAAGCTGAACAAG 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401	Oy 1332 uTyrLeuAspSerYalAsnGluThrGlnPheCysValAsnIleProAlaValArgAs 1351	1302 nLeuLeuSerGlyPheMetValProSerGlu	Db 4108 AGATCAACTCACCTGTAATAAA	Db 3988 GGAATCTGCCAGCCTCCTGCGATCAGAAGAGAGACCAAGGAAAATGAGGGTTTCACAGTCAC 4047 Qy 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249

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School Schilarity; 91.00 MacChes Secretic Schilarit	ERENCE/DOCKET NUMBER: 102286.377 COMMUNICATION INFORMATION: EPHONE: (617) 526-6000 EFAX: (617) 526-5000 ITION FOR SEQ ID NO: 2: NCE CHARACTERISTICS: GTH: 5056 base pairs E: nucleic acid ANDEROMS: single OLOGY: linear ULE TYPE: cDNA 271-2 SCORES: 4 4448-88 LEGATO.
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652 ABBGIYVALTYLABPARN	555 PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu
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3104 ACGCCACGGTCATCGCTTGCATTÁCCTGGATGANACGGACÁTGGGAGAAGTTCGGC 3163 950 LysGlulysAlaLeuSerPheMetArgGlnGlyfyrGlnArgGluLeuLeu 966 3164 CTAGAGAAGCGGCAGGGGCTTTGGAGCTGATAACAGCGAGGTGACACCCAGCACC 323 967 TYCGInArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986 3224 TTCAGACAACCCAGCTCTGCCTTTGCGGCCTTCTGTGAAACGGGCACCCAGCACC 3277 987 TTCLEUSErAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006 [ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer CTAAAAGACCGCTGCAGGAAGTGGAAGTCAAGGCTGCTGTCTACCATCATTTCATCAGT AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln SerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu :::: GCTGTTCGCACCCTGGATCCAGAAGGTCGTGGCCGGAAGGAATCAGAATGAAAACTGTG SerPheSerPheProProAsnThrValThrGlySerGluArg GACATCCACCTTGGATCCAGAACGCCTGGGCCGTGAAGGACCGAGATCTGAGAAGAG SerPheSerPheProProAsnThrVal

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                                                                                                                                                                   Sequence 23, Application US/09142334 Patent No. 6268485 GENERAL INFORMATION:
           APPLICANT: Farries, Timothy C.
APPLICANT: Harrison, Richard A.
APPLICANT: Harrison, Richard A.
TITLE OF INVENTION: Down-Regulation Resistant
FILE REFERENCE: 4-30443/h/IMU/PCT
CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
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OF SEQ ID NOS: 35
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SEQ ID NO 23
; LENGTH: 5067
; TYPE: DNA
; ORGANISM: Homo sap:
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                                          LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr
                                                                                         TCTCAGAACCAGCTTGGCGTCTTGCCCTTGTCTTGGGACATTCCGGAACTCGTCAACATG
                                                                                                                                                                                                                                                                                                                                           SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGln---TrpLeuSer 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro
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                   TTCTACTACATCTATAACGAGAAGGGCCTGGAGGTCACCATCACCGCCAGGTTCCTCTAC
                                                                                                                                                                                                        GlyAspTrpSerIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSer
                                                                                                                                                                                                                                                                                 GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu
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Db 2659 CTCCACAATCCAGCCTTCTGCAGCCACCACAGAGGCGTCĂC 2706 Qy 805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgpro 824 :::: ::: ::: :::	2485 A: 747 P: 2542 Q: 767 Q: 2602 Q: 786	Oy 681 GlySerSerPrOHisVal696	652 AspGlyValTyrAspAsn	Db 1966 GCCGGTGTCTTCTCCGACGCAGGGCTGACCTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	

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MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSer TTTCTGACC	1062 TyrGlnProAsnIleAspValGlnGluSerIleHis	1007 GlnAsnValLeuHisAxgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGly 1025	950 LysGluLys	895ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly 910	2827 GACGGTGTCAGGAAGTCCCTGAAGGTCGTGCCGGAAGGAA
FEGULA NO. 3282300 FEGURA NO. 3282300 APPLICANT: VOCEL, CARL-WILHELM APPLICANT: BREDEHORST, REINHORST APPLICANT: KCCK, MICHAEL APPLICANT: FRITZINGER, DAVID TITLE OF INVENTION: RECOMBINANT PROCVE NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON STATE: VA COUNTRY: USA ZIP: 22202 COMPUTER READABLE FORM:	Oy 1371 GArgGInAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAs 1388	CTCCGA SVALAS ::: TCTAGC rIleVa ::: GGTCTA	1269 aVal	3999 GGAATCTGCCAGCCTCCTGCGATCAGAAGAGACCAAGGAAAATGAGGGTTTCACAGTCAC 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe	Qy 1186 ValalaLeuLysalaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsn 1204 ::: :::::: Db 3880 ATGGTGTTCCAAGCCTTGGCTCAATACCAAAAGGACGCCCCTGACCACCAGGAACTGAAC 3939 Qy 1205 IleGlnValThrValThrGlyProSerSer

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Query Match:
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TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5948 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TTCTTC---TGGCCTTACAATTTACCAGACCTTGTCAGTTTGGGGGACTTGGAGGATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 GCCAAATATGAACATTCCCCAGAGAATTATACTGCATATTTTGATGTCAGGAAATATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724 ---GAAAATTTCCACGTGTCTATCACTGCAAGGTACTTGTATGGAGAGGAAGTGGAAGGT
                                                                                                                                                                                                                         LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLys--- 511
                                                                                                                                                                                                                                                                                                       TATTTCAAGCCAGGAATGCCATATGAACTGACGGTGTATGTTACCAACCCTGATGGCTCA
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                                                 ProLysAlaCysValIleValTyrTyrIleGluAspAspGlyGluIleIleSerAspVal 546
                                                                                                                                                                                  CAAACCCAGGGAGGATCTGGAAACTATCTTCATGTAGCCATTACATCTACAGAGATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCCTGAACATACCATTGAATGCTCAA-----AGCCTACCAATCACTGTTAGAACT 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CATTCTATGGGAACCACTTTGAGTGATGGGACTGCTAAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAGCGGCATTCATATTGTGGCATCTCCCTATCAGATCCACTTCACAAAAACCCCCCAAA 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro 318
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                   CCTTCCTTCCGGTTTGTGGCTTACTACCAAGTGGGAAACAACGAAATTGTGGCTGATTCT 1608
                                                                                                                                         -----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTrpThr 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458
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                                                                                                   CCCAGGAGAGATGGGCAGATCTGGTGACCATGAATCTGCATATCACTCCAGATCTCATC
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THEGLYTYTYLEUGLYMET PHEMETARGCTANGCTTANGATATTGGGACACCATATAGAANAGATTTAGCCAACCTTANGATTATGCACACTATAGAANAGATTTAGCACACCATATAGAANAGATTTAGCTTTAGAGATTAGAANAGATTTAGAANAGATTTAGAANAGATTTAGAGATTAGCACACCATAATCTCAGAATTTCAGCAGTTGGATTTGAGAGTGTTTTGAGAGTGTTTTGAGAGTGTTTGAGAGTGTTTGAGAGTGTTTTGAGAGTGTTTGAGAGTGTTTTAGAGAATCCTAAATCTCAAAATCTGAAAATCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTCAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTGAAAATGCTTGAAAATGCTGAAAACCCCCCCC	547 LeuLysIleProValGln
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2806 AAAGGATTGGTGGAACACAGCTNGATGATCANAGCCGGCANATTAGATGACAGAGTC 2865 855 PROPAGABITIA'SITHCOLYSETGILARYSIACIAILETTATATATGACAGAGTGACCAGATTATTAGATGACAGAGTTATTAGATGACAGAGTTATTATTAGATGACAGATTATTAGATGACAGATTATTATTAGATGACAGTTAGATGACCTGTGGCTCAGATTATT 2925 905 GLYPTGSETILASAGLY	

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RESULT 8
US-09-017-947-1
Sequence 1, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: WOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORS:
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                                                                                                                                                                                                                                                             TTACAAATTGAAAAAGCCTGCGAGACGAATGTGGATTATGTCTACAAAACCAAGCTGCTT
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  VOGEL, CARL-WILHELM BREDEHORST, REINHORST
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                               CysProSerGlnValThrValLysAla------GluLeuLeuLysThrAlaSer 67
                                        GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys 127
                                                                                ATAGAGATTCCAGCAAAAGAAGTGAGTACGGACTCCAGGCAAAATCAATATGTGGTTGTG 321
                                                                                                                                                                                                            AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87
                                                                                                                                                                                                                                                                                                                                                                                      ProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaAlaLeuAlaVal-------AlaProGlyProArgPheLeuValThrAla 32
                                                                                                                          LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107
                                                                                                                                                                                                                                                         ACTCCAAAACAGCTTGACATCTTTGTTCATGATTTTCCACGGAAGCAGAAAACCTTGTTC
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1156CATTCTATGGGAACCACTTTGAGTGATGGGACTGCTAAGCTC 1197 419 ABRTYTHTVAlProGInSerGlyThrPheLyBIleGluPheProIleLeuGluAbpSer 438 1198 ATCCTGAACATACCATTGAATGCTCAAAGCCTACCAATCACTGTTAGAACT 1248 439 SerGluLeuGlnLeuLyBAlaTyrPheLeuGlySerLyBSerSerMetAlaValHiBSer 458 11249 AACCATGGAGACCTCCCAAGAGAAACGCCAGGCAACCAATGACGCCATAGCCTAC 1308 459 LeuPheLyBSerProSerLyBThrTyrIleGlnLeuLyBThrArgAbpGluAbnIleLyB 478 11309 CAAACCCAGGGAGGATCTGGAAACTATCTTCATGTAGCCATTACATCTACAGAGATTAAG 1368	CAAAGCGGCATTCATATTGTGGCATCTCCCTATCAGATCACATAAACCCCCAAA ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	MetLysAsnvalMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro ::::::: TTCCGTTCTCGATTTCCAAATCTCAATGAGCTTGTTGGGCATACTCTGTATGCATCT GlyProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnVal :::	243 SerLysHisleuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly 262 :::::::::::::::::::::::::::::::::::	188 ValileSerLysThrPheGlnLeuSerSerHisProlleLeuGlyAspTrpSerIle 206 :::	128 ArgileSerValPheileGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys 147 382TTTCTGTTTATCCAGACAGATAAAGGCATCTATACACCAGGTCTCCAGTACTC 435 148 PheArgileValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu 167 ::: ::: 436 TATCGTGTTTTTCTATGGATCACAACACAAGCAAGATGAACAAAACTGTGATTGTTGAG 495 168 IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAspLeuGly 187 ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
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679 SerLeuGlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697	2062 ATGGGGTACACTTGTGAAAAGCGTGCAAAATACATCCAGGAGGAGATGCTTGTAAGGCT 2121 650TyrIleAspGlyValTyrAspAsnAlaGluTyrAla 661 2122 GCCTTCCTTGAATGCTGTCGCTACATCAAGGGGGTCCGAGATGAAACCAACGGGAGAGC 2181 662 GluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPhe 678	1942 CCTGCAAATCGGAGGCGTCGCAGTTCTGTTTTGCTGCTGCAAGATGTCATGCATG		CCTTCCTTCCGGTTTGTGGCTTACTACCAAGTGGGAAACAAAC	479 ValGlySerPropheGluLeuValValSerGlyAsnLysArg 492

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LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallIeHisSerGlu LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallIeHisSerGlu Liiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii		LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	2401 ATCTGTGTGGCTGAACCTTATGAAATAAGAGTCATGAAAGTCTTCTTCATTGATCTT 2457 753 ASBLEUProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsb 772 : :
Qy 1337 ValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysValSer	Qy 1253 ArgArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGlu 1272	Qy 1129 SerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAla 1148 3607GAAGAATACAATGCTCACACCCACAACATTGAAGGCACTTCCTATGCC 3654 Qy 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168	Db 3460 AAGAAGGCCACAAATTATTTACTCAAAAAGTATGAGAAACTGCAAAGGCCTTACACT Qy 1089 LeualaLeuIleThrTyralaLeuSerSerValGlySerProLysalaLysGlualaLeu

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Best Local Similarity:
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TELEPHONE: (703) 413-2220
TELEPAX: (703) 413-2220
TELEX: 240855 OPAT UR
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 5924 base pairs
TYPE: nucleic acid
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Patent No. 5773243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FRITZI
APPLICANT: BREDEH
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRITZINGER, DAVID C. APPLICANT: BREDEHORST, REINHARD APPLICANT: VOGEL, CARL-WILHELM TITLE OF INVENTION: DNA ENCODIN NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: ur
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MEDIUM TYPE: Floppy
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LOCATION:
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                               339 SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 CysProSerGlnValThrValLysAla------GluLeuLeuLysThrAlaSer
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                                                                                                                                          TTCCGTTCTCGATTTCCAAATCTCAATGAGCTTGTTGGGCATACTCTGTATGCATCT---
                                                                                                                                                                                                                                                                                                                        AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle-----
                                                                                                                                                                                                                                                                                                                                                                                  SerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly
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                                                                                                                                                                          MetLysAsnValMetAspSerSerAspGlyLeuSerGluTyrLeuAspLeuSerSerPro
                                                                                                 GlyProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnVal
                                                                                                                                                                                                                   TCACTCACGAGAATTCCGATTATTGATGGAGATGGGAAAAGCAACACTAAAAAAGAGATACA 897
                                                                                                                                                                                                                                                                                        ---GTGGCCTTTGTCCTCTTTGGAGTGAAAATAGATGATGCTAAAAAGAGTATTCCAGAC
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                                                                                                                                                                                                                                                   -----ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGlu 298
                                                                                                                                                                                                                                                                                                                                                             ---GAAAATTTCCACGTGTCTATCACTGCAAGGTACTTGTATGGAGAGGAAGTGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCCAAGCTTTGAAGTCCGTCTGCAACCATCAGAGAAGTTTTTTTACATTGACGGCAAT
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                                                                       -GTAACAGTCATGACAGAATCAGGCAGTGATATGGTAGTGACTGAG
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Qy 960 GlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsn 979	Qy 940 ThrLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGln 959		Qy 905 GlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGly 922 ::	885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu	871 ABRATGLEUGINSETTHYLEULYSTHYLEUSEYPHESEYPHE	851 VallysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp	Qy 831 ProlleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu 850	Qy 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIle 830	Qy 793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	Qy 773 TyrLeuLysAspAlaThrGluValLysVallleIleGluLysSerAspLysPheAspIle 792	Qy 753 AsnLeuProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772	AT:	Qy 713 ValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly 732 ::: ::: Db 2341 CTGAGGGATTCCATCACAACCTGGGTGCTGGCTGTAAGCTTTACACCCACC	Qy 698AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThr 712 ::: Db 2281 AAGGACTTGACCGAGGAGCCTAACAGTCAAGGGATTTCAAGCAAG	Qy 679 SerLeuGlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697	Qy 662 GluargPheMetGluGluasnGluGlyHisIleValAspIleHisAspPhe 678	650 2122 GC	649 2062 AT

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1287 SerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGly 1306 :::	1273 ABRLYBASDABDLeuABRHISValABDLeuABRValCySThr 1286	1253 ArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGlu 1272	1233 PheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSer 1252	1219AlaValValGlnProMetAlaValAsnIleSerAlaAsnGly 1232 ::: ::: ::: 3895 CTCCTGGCTCGGACAGTAGAGACCAAAACTCAACACATCACTGTGACAGCATCAGGT 3954	1208 ThrValThrGlyProSerSerProSerProLeu	1189 LysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnVal 1207	1169 SerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeu 1188 	1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168	1129 SerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAla 1148 ::: ::	1109 ABNMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpVal8erSerGlu 1128		069 GlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnfyrThr		TTCTGGTT	LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallHisSerGlu	999 ALAASPPYOTYTITEASPILEASPGINASNYAILEUHISATGTNYYYTNYTYPINTTYPEU 101/ 	TyraspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluCGTGCATCTAGTTCTTGGCTAACAGCATATGTCGTAAAAGTCTTTGCCATGGCTCGTGCATCTAGTTCTTGGCTAACAGCATATGTCGTAAAAGTCTTTGCCATGGCT	::::::: ::::: ::::::
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IOR APPLICATION DATA:

APPLICATION NUMBER: US 08/043,747

FILING DATE: 07-APR-1993

TORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5773243man F.

REGISTRATION NUMBER: 24,618

REPERENCE/DOCKET NUMBER: 1126-101-0

LECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEPAX: (703) 413-3220

TELEFAX: 24885 OPAT UR

RMATION FOR SEQ ID NO: 75:
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DIUM TYPE: Floppy disk
MPUTER: IBM PC Compatible
BRATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patentin Release #1.0, Version #1.25
ENT APPLICATION DATA:
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ESPONDENCE ADDRESS:
DELON, SPIVAK, McCLELLAND, MAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICANT: FRITZINGER, DAVID C. ICANT: BREDEHORST, REINHARD ICANT: VOGEL, CARL-WILHELM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 TTCATTCAGCCAGGATCAGTCAAGGTGTACAGCTACTACAATCTAGATGAAAAATGTACC 4410
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                                                                                                                                                                                                                                                                                                                             LICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r: 1755 S. Jefferson Davis Highway, Suite 400
Arlington
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| TGCCGATGTGCAGGAGAAACCTGTTCCTCGCTCAACCATCAGGAAAGGATTGATGTTCCA 4530
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Best Local Similarity:
Query Match:
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LENGTH: 4138 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                            AAAGGGAAGATTTTCAAGGTTGGCAGGCAACACAGGGGAGATGGGGAGAATCTGGTGACC
                                                                                                                                                                                                                                                                                                          ArgGlyGlnLeuValAlaValGlyLysGlnAsnSer------Thr 515
                                                                                                                                                                                                                                                                                                                                                                       ValSerGlyAsn------LysArgLeuLysGluLeuSerTyrMetValValSer 502
                                                                                                                                                                                                                                                                                                                                                                                                            CATGTAGCCATTACATCTACAGAGÁTTAAGCCCGGAGATAACTTACCTGTCAATTTCAAT
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                                             TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582
                                                                                                                                                                   TyrileGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln-----
                                                                                                                                                                                                             ATGAATCTACATATCACTCCAGAT----CTCATTCCTTCCGGTTTGTGGCTTAC
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                              1734 GAGGTTACAGCAAGTGTCCAGGGAGAGTTGATGTCAGATGGTGTGAAGAAGAAACTGAAA 179:
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851 ValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp 870
                                                                                                                                                                                                                                                                                                              AsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn
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                                                                                                                       GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly------GluIle
                                                                                                                                                                GCTTCCACAGAAAGTCAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer
                                                            ProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu
                                                                                              CTGTCCTCCAGGGCAGTATCGTTTGTGATAGTCCCATTAGAGCAAGGATTGCATGATGTT
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                                                                                                                                                                                                                             TACGCTGACAAGGATATTTATGTACGAGTGGAACTGTTATACAGCCCAGCCTTCTGCAGT 1625
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2034 GAGCAAATATGATCCGCATGACTGCACCAGTTATTGCCACCTACTACCTGGACACCACA 209:
nAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluAr 1202
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                                                                               TCCTGTAGTCCAATGGCTGATAGATCAGCAATATTATGGGGGAACATATGGACAAACCCA
                                                                                                                  eProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGl
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                                                                                                                                                                                                                                                                                                                                      nPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIl
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GENERAL INFORMATION:
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Patent No. 5922320
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatibl
OPERATING SYSTEM: PC-DOS/N
                                                                                                                                                                                                                                                                                                              APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
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                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                            ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                    CITY: ARLINGTON
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BREDEHORST, REINHORST
KOCK, MICHAEL
  PC-DOS/MS-DOS
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Qy 535 TyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln 552	Qy 516 MetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTyr 534	Qy 503 ArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThr 515	Qy 487 ValSerGlyAsnLyBArgLeuLySGluLeuSerTyrMetValValSer 502	Qy 469 GlnLeuLysThrArgAspGluAsnIleLysValGlySerProPheGluLeuVal 486 :::	Qy 449 GlySerLysSerSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle 468	Qy 429 LysileGluPheProlleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu 448	Qy 409 AsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428 ::: ::: Db 204 ACCACTTTGAGTGATGGGACTGCTAAGCTCTTCCTGAACACACCACAAAATGCTCAA 260	Qy 389 ValVallleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGly 408	Oy 369 ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsn 388 ::: ::: Db 126 ACGGTGTATGTTACCAAACCTGATGGCTCACCAGCTGCC	Qy 349 TyrileileGluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAla 368	US-10-020-095-4 (1-1428) x US-08-662-227-33 (1-4138)	10.46% Indels: 2 Gaps:	: 6.68e-71 768.50 imilarity: 41.88* 1 Similarity: 24.74*	MOLECULE TYPE: 3-662-227-33 nment Scores:	; LENOTH: 4138 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear	; TELEPHONE: 703-413-3000 ; TELEPAX: 703-413-2220 ; INFORMATION FOR SEQ ID NO: 33: ; SEQUENCE CHARACTERISTICS:		CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:	CORRENT APPLICATION DATA: CAPPLICATION NUMBER: USC/08/662,227	; SOFTWARE: PatentIn Release #1.0, Version #1.30
B &	d S	S B 8	S & &	P Q	Db Q	Db Qy	9 g	S B &	S B &	Db Qy	Db	. S	Qy dd	dg Q	Qy db	g Q	dd Ag	Db	Ŋ.	da
793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	1566 TACGCTGACAAGGATATTTATGTACGAGTGGAACTGTTATACAGCCCAGCCTTCTGCAGT 1625	ASILEMPROTYRSERVELLIERIGGLYGIUGURERALIEMGULIEURILIERIRELIERIGEN	GGGATCTGTGGCTGAACCTTATGAAATAACAGTCATGAAAGACTTCTTCATTGATCTT	O TrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuThrThrThr	700 AssMetGlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSer 719 :::		1242 GCAAGAAGTGATTTGAAGATGATTTATTTGGAGAAGGTAACATCACCTCAAGGTCT 1298	TGCTGTCACTACATCAAAGGGATCCAAGATGACAATAAACGGGAGAGCGAGTTGTTTCTG	658 AlaGluArgPheMetGluGluArnGluGly	648			643 AspAlaAsnLeuThr 647 942 AGCACTAATCTCAACACCAAACAGAGATCAGCTGCAAAGTGTCCTCAGCCTGCAAATCGG 1001	623 LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThr 642	603 ASNASDIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyr 622	583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602 :::	563 TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582	TGCATGGGAACGTTGGTTGAAAGGAGCGACTTCCAGAGACAATCGAATACAAATG	553LeuValPheLysAspLysIleLysLeuTyr 562	609 TACCAAGTGGGAAACAATGAAATTGTGGCTGATTCTGTCTG

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1085 ABDABNTYTThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLy8Ala 1104		813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIle 830
US-09-017-947-33 ; Sequence 33, Application US/09017947 ; Patent No. 6303754 ; Patent No. 6303754 ; Patent INFORMATION: GENERAL INFORMATION: APPLICANT: WOGEL, CARL-WILHELM APPLICANT: KOCK, MICHABL APPLICANT: FRITZINGER, DAVID ITILE OF INVENTION: RECOMBINANT PROCVF ; NUMBER OF SEQUENCES: 39 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,	5 W	Qy 1142 eGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyI1 1162

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 4138 base pair
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STRANDEDNESS: single
TOPOLOGY: linear
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CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                                                   GlnLeuLysThrArgAspGluAsnIleLysValGlySer----ProPheGluLeuVal
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-ProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu
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Best Local Similarity:
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Sequence 3, Application US/09241606
Patent No. 6472140
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
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SEQ ID NO 1
LENGTH: 339
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APPLICANT: Gonias, Steven L.
TITLE OF INVENTION: Transforming Growth Fa
FILE REFERENCE: 00370-02
CURRENT APPLICATION NUMBER: US/09/311,352B
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 6
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ORGANISM: Homo
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DB:
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SEQ ID NO 3
LENGTH: 750
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CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
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LOCATION: (1)..(750)
OTHER INFORMATION: A /LRP Binding
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ORGANISM: Homo sapiens
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                     CTCAAACCAGCCATAGTGAAAGTCTATGATTACTACGAGACGGATGAGTTTGCAATCGCT
                                                  ThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAlaValArg 1376
                                                                                                                                                                                                                          GATGTGAAGATGGTCTCTGGCCTTCATTCCCCCTGAAGCCAACAGTGAAAAATGCTTGAAAGA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCATGAAAGTGACAGGAGAAGGATGTGTCTACCTCCAGACCTCCTTGAAATACAATATT
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                                                                                                                    ValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysValSerAsn 1356
                                                                                                                                                        TCTAACCATGTGAGCCGGACAGAAGTCAGCAGCAACCATGTCTTGATTTACCTTGATAAG
                                                                                                                                                                                    SerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSer
                                                                                                                                                                                                                                                                                                                            AsnValCysThrSerPheSerGlyProGly-----ArgSerGlyMetAlaLeuMet 1299
                                                                                                                                                                                                                                                                                                                                                                  GCTTTAGGAGTGCAGACTCTGCCTCAAACTTGTGATGAACCCAAAGCCCACACCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                AspValAlaValLys-----GluAsnLysAspAspLeuAsn---HisValAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeu
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Db 712 GAGTACAATGCT 723

Search completed: January 17, 2004, 01:18:53
Job time: 445 secs

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Result
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        Score
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                                                                                                                                                                                                                                                          January 17, 2004, 01:19:00 ; Search time 982 Seconds (without alignments) 5125.623 Million cell updates/sec
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ALIGNMENTS

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RESULT 2
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US-10-108-260A-953
; Sequence 953, Application US/10108260A
; Sequence 953, Application US/2004008560A1
; Publication No. US20040005560A1
; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
CTILE OF INCENTION: NO. US20040005560A1e1 full ler
FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 953
; LENGTH: 2273
; TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 7, Application US/10292081A
Publication No. US20030162202A1
GENERAL INFORMATION:
APPLICANT: Kenneth David Becker
APPLICANT: Gonul Velicelebi
APPLICANT: Xin Wang
APPLICANT: Randolph E. Tanzi
APPLICANT: Lars Bertram
APPLICANT: Aleister J. Saunders
                                                                                                                                                                                                                                                                   RESULT 3
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             APPLICANT: LAYS BETTYAM
APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
   SOFTWARE: FastSEQ for Windows Version
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LENGTH: 4576
TYPE: DNA
ORGANISM: Homo :
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                                                                                                             LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp
::: :::||| ::::::
                                                                                                                                                                           TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer :::||||||||||||||||| :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ### SAGGACAGTCTGGTCTTGTCCAGACAGACAATCAATCTACAAACCAGGGCAGACAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
                                                                                                                                                                                                                                                 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
                                                                                                                                                                                                                                                                                    GTGGCCTCAAGCAATTTTCCTTTTTCCCCTCTCATCAGAGCCCTTCCCAGGGCTCCTACAAG
                                                                                                                                                                                                                                                                                                         LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer
                                                                                                                                                                                                                                                                                                                                                                    LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle
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                               GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA
                                                              ValThrLeuThrPheLeuProLeu--
                                                                                             GAAGAGATGAATGTATCAGTGTGGGCCTATACACATATGGGAAGCCTGTCCCTGGACAT
                                                                                                                                                           TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMet 599		541 GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560	521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540 1630 GTGAAGTCAGACATTGCTCCTGTCGCTCGGTTGCTCATCCTATCCTATCCTACCTA	511LysGlnAsnSerThrMetPheSerLeuThr 520	493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478	439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458	429 LysileGluPhePro	412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428	392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411	372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391	352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351. :::	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	892 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA 951
Qy 877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896 :::	Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876	G 1	83 ThrValThrAlaLeuSer	813 GluAspGlyAlaThtValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	798 G 2566 G	778 T 2506 A	Qy 758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777	≽ —н	Oy 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737	⊣ ≽	ı Q	661 AlaGluA 2167 GAGTCAG	652 ABPGIYVAITYKASPASRALAGIU	632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyr	617 T 1987 T	Qy 603AspasplleThrMetGluAsnValValHisGluLeuGluLeu 616	Qy 600 602 :: Db 1867 CCTGATGCTGAGCTCTCGGCGTCCTCGGTTTACAACCTGCTACCAGAAAAGGACCTCACT 1926	1810 GCTCCTCAGTCCGTCTGCGCCCTCCGTGCTGTGGACCAAAGCGTGCTGCTCATGAAG

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                                                               SerProLeuAlaValValGln-----
                                                                                                                                                                                                                                                                                                              GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysalaLeuSerGluPheAla 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGlyIlePro------IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175
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ACATTTTCCAGCAAATTCCAAGTGGACAACAACAGCGCCTGTTACTGCAGCAGGTCTCA 3954
                                                                                                                                                                            GAGGACCTGACCTCTGCAACCAACATCGTGAAGTGGATCACGAAGCAGCAGAATGCCCAG 3777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGACATCCTATGTGCTCCTCGCT---TATCTCACGGCCCAGCCAGCCCCAACCTCG
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RESULT 4
US-10-052-817-1
; Sequence 1, Application US/10052817
; Publication No. US20020114792A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovaces, Dora
; APPLICANT: Kovaces, Dora
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOVAGE, DOTA
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and
TITLE OF INVENTION: Alzheiner's Disease
FILE REFERENCE: 0609.4460005
CURRENT APPLICATION NUMBER: US/10/052,817
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: 09/241,606
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: 09/148,503
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/093,297
PRIOR APPLICATION NUMBER: 60/093,297
PRIOR APPLICATION NUMBER: 09/093,297
PRIOR APPLICATION NUMBER: 09/093,297
PRIOR APPLICATION NUMBER: 00/093,297
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PRIOR PRILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PAtentin Ver. 2.0
                     Alignment Scores: Pred. No.:
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                                                                                                  US-10-052-817-1
                                                                                                                    NAME/KEY: sig peptide
LOCATION: (44)..(112)
NAME/KEY: CDS
LOCATION: (44)..(4468)
NAME/KEY: mat peptide
LOCATION: (113)..(4468)
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGTCTTGATTTACCTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT
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2.83e-133
1441.00
Length:
Matches:
4577
451
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for

Qy 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316 	Qy 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	Qy 272SerPheTrpGlyLys 276	Qy 264 ValThrLeuThrPheLeuProLeu		224 IVEBS GLOUBERT LONGER LONG	656 GTGGTGGTACAGAAGAAATCAGGTGGAAGGACAGAGCACCCTTTCACCGTGGAAGAA	Qy 206 IleGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 20	Qy 167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 ::: ::: ::: Db 536 GTATACATTCAGGATCCCAAAGGAAATCGCATCGCACAATGGCAGAGTTTCCAGTTAGAG 595			127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal	OY 10/ InrujyarginiginaspgiulleLeuPneSerAsnserIhrargLeuSerPneGiuThr 126	311GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG	Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgYal 106	OY 72SerValleuGliAlaGiuGlyValPheGluLySGlySerPheLysThrLeuThr 89	203 CTG	Qy 52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71	Db 146 GTCCCTCCTGCTCCACACTGAGACCACTGAGAAAGGGCTGTGTCTCTGAGCTAC 202	86 CIVITAGICCICCIGCCCALAGACGCCICAGICICTGGAAAACCGCAGIATATGGTTCTG 1 32 NlaDroGlyTlaTlaArgBroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyTlaTlaArgBroGlyGlyBlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalGlyMalGlyMalGlyTavicacGroGlyGlyAegUsl#hrTlaGlyMalG	12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr	US-10-020-095-4 (1-1428) x US-10-052-817-1 (1-4577)	19.61%	Percent Similarity: 46.20% Conservative: 266 Best Local Similarity: 29.06% Mismatches: 551
Db 192				Db 169	рь 163 Qy 54	рь 157 Оу 52	Qy 51	Оу 45 рь 151		Db 139	0у 45	Db 136		Qy 43				Db 11:		Qy 3:	Db 100			Db 98
	CCTGATGCTGAGCTCTCGGCGTCCTCGGTTTACAACCTGCTACCAGAAAAGGACCTCACT	GCTCCTCAGTCCGTCTGCGCCCTCCGTGCTGGACCAAAGCGTGCTGCTCATGAAG	::: ::::::: ::::::: ::::::	1691 GACGTGATTGGGGATTCTGCAAAATATGATGTTGAAAATTGTCTGGCCAACAAGGTGGAT 1750 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	1631 GTGAAGTCAGACATTGCTCCTCGCTCGCTCGCTCGTCTATCTA	1571 ACTCATGGACTGCTTGTGAAGCAGGAAGACATGAAGGGCCATTTTTCCATCTCAATCCCT 1630 521 ProGluAsnSerTrpThrProLysalaCysValIleValTyrTyrIleGluAspAspGly 540	MetPheSerLeuThr	493 LeulysGIULeuSerTyrMetValValSerArgGlyGInLeuValAlaValGly 510 493 LeulysGIULeuSerTyrMetValValSerArgGlyGInLeuValAlaValGly 1510 CTGAAGAAGCTCTCCTTTTATTATCTCATAATGGCAAAGGGAAGGGAAGTGTCCGAACTGGG 1570	TGTGGCCATACTCAGACAGTCCAGGCACATTATATTCTGAATGGAGGCACCCTGCTGGGG	1391 CTTGTGTTCTCCCCAAGCAAGAGCTTTGTCCACCTTGAGCCCATGTCTCATGAACTACCC 1450	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478	439 SerGluLeuGInLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458		429 LysileGluPhePro	MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe		ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	372 ValThrArgAlaAspClyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValIValIle 391 	CCCTTCTTGGGCAG	352 GluphepheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371	332 INTOLYTIESETATGASHVALESETHTASHVALEDEPOEDYSGIHTISASDTYTLELLE 351		317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	989 TATGAAATGAAA 1024

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QY 937 Db 3005 QY 957 Db 3065 QY 977 Db 3125 QY 995 Db 3185 QY 1015 Db 3245 QY 1035 Db 3305 Db 3365 QY 1108 Db 3425 QY 1108 Db 3542 QY 1113 Db 3542 QY 1113 Db 3542 QY 1113 Db 3542 QY 1113 Db 3719 QY 1123 QY 1126 Db 3839 QY 1239 QY 1239 QY 1239 QY 1239 QY 1239 QY
37 ABDTYTLeuThrLysLyslysdinLeuThrAspAsnicutlysGluLysAlaLeuSerPhe 956 63 GRITACCHANTGANACKAGGCCCTTCTCCGGGGCTCAGGCCCTTGGCTTT 3064 65 GREATSCINALTGANACKAGGCCTTCTCCGGGGTTAGGCTTAGGCCTTTGGCTTT 3064 65 GTCANCACTGGTTACCAGAGACTGGCTTGAACTACAACACTATGATGGCTTCTGGCTTT 3064 65 GTCANCACTGGTTACCAGAGACTAGGTCAACTACAACACTATGATGGCTCCTACAGCCCTTTGTTCTGAG 3124 65 ACTTTGGCCCAGCTCAACCAGGCAACCAGGCAACACCAGGCAACACCAGGCAACACCAGGCAACCAGGCAACCAGGCAACACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCACATTCCCTCCAAGCCCTTCTTCTCAAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCAACCAGGCACACTTCTCCCAAGCCCTTCTTCTCCAAGCCCTTCTTCTCCAAGCACCAGGCAACACAGGCAACAACCAGGCAACACACTAGACCAGACCACATACACCAGGCAACACACTAGACCAAGACAACACAGACACAACACACAC

72SerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThrLeuThr 89	Qy 52 CysProSerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrVal 7.	Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31	Gaps: -873-403-4 (1-4422)	No.: 3.36e-133 1t Similarity: 46.20% No. 25 Similarity: 29.06%	; ORGANISM: Homo sapiens US-09-873-403-4	; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ 1D NO 4 ; LENGTH: 4422 ; TYPE: DNA		9-178 NUMBER: US/ : 2001-06-0 UMBER: 09/62	; GENERAL INFORMATION: ; APPLICANT: STIVETAVA, Pramod K ; TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC ; TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY	RESULT 5 US-09-873-403-4 ; Sequence 4, Application US/09873403 ; Patent No. US20020028207A1	Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380	QY 1349 ValargasnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368 ::::::::	Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348 ::: :: Db 4283 CATGTCTTGATTTACCTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT 4342	Qy 1312 GluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1328	Qy 1293ArgSerGlyMetAlaLeuMetGluValAmnLeuLeuSerGlyPheMetValProSer 1311		:::
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392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411	372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391		332 TIREGITI ESSERATGASHVALSSETHRASHVALPHSPHSLYSGIRHISASDIYTILELLE 351	SEFFICIAL PROPERTY AND	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	272SerPheTrpGlyLys 276	264 ValThrLeuThrPheLeuProLeu	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: :: ::::	224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	167 LeuIleLybaspProLybSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166	127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146 ::: ::: ::::	107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	90 LeuProSerLeuProLeuAsnSerAlaAspGlu1leTyrGluLeuArgVal 106 	:::

GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu		ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle :::::	PheMetAgnSerPheAla :::::: TAITTAATTGGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC	G1yTyrTyrLeuglyMet		ThrGlnDroAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	LeuTyrTrpSerLy8ValLy8AlaGluProSerGluLy8ValSerLeuArgIleSerVal	y 541 GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560 	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly ::::::	y 511LysGlnAsnSerThrMetPheSerLeuThr 520	LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	ValGlySerProPheGluLeuValValSerGlyAsnLysArg 	LeuPheLysSerProSerLysThrTyr1leGlnLeuLysThrArgAspGluAsn1leLys	439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458	Y 429 Ly8IleGluPhePro	1153 TTCATCAGAGGAAATGAAGCAAACTATTACTCCAATGCTACCACGGATGAG 1203 / 412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428
Qy 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallle 1034	Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014	Qy 977 PheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArg 994	Qy 957 MetargGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976	Qy 937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956	Qy 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936	Qy 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916 :::::: ::: :::::: Db 2842 GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCCAG 2901	Qy 877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896	Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876 ::: ::: Db 2731 GAGAAGGAAACAACATTCAACTTCCCTACTTTGTCCATCAGGTGGTGAGGTTTCT 2784	Qy 842SerAspAlaValThrGlnMetIleLeuValLysalaGluGlyIle 856	Qy 833 ThrValThrAlaLeuSer	GluaspGlyAlaThrValleuPheProlleargProThrHisLeUGlyGluileProlleACTGTGTCCTGGGCAGTAACCCCAAAGTCATTAGGAAATGTGAATTTC	798 Glu	Qy 778 ThrGluValLysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	Oy 758 VallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777	Qy 738 ThrProValGluLeuGlnAlaPheGlnProPhePheItePheLeuAsnLeuProTyrser 757		698 2227

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                                            4240 CATGTCTTGATTTACCTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT
                                                                                                                                                                                     1312 GluAlaIleSerLeu------SerGluThrValLysLysValGluTyrAspHisGly 1328
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                                                                                                                                                                                                                                                            ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer
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                                                                                          LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla
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CURRENT APPLICATION NUMBER: US/09/873,403
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/625,139
PRIOR FILING DATE: 2000-07-25
PRIOR PELICATION NUMBER: 60/209,266
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4577
TYPE: DNA
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Best Local Similarity:
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APPLICANT: Srivetava, Pramod K
TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN
TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY
FILE REFERENCE: 8449-178
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Patent No. US20020028207A1
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                                                                                                                                                                 311 -----GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG
167 Leu---IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185
                                                     476 AAATTTCGTGTTGTCTCCATGGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA
                                                                                                        147 LyspheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle
                                                                                                                                                                                       127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146
                                                                                                                                                                                                                                                                            365 AAAGGACCAACCCAAGAA-----TTTAAGAAGCGGACCACAGTGATGGTTAAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     90 LeuProSerLeuProLeuAsnSerAlaAspGlu------IleTyrGluLeuArgVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal
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479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 	LysIleGluPhePro	MetGluAlaValGlnLysileAsnTyrThrValProGlnSerGlyThrPhe	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	LysLysAsmIleThrLysThrPheLysIleAsmGlySerAlaAsmPheSerPheAsmAsp 		ValThrleuThrPheLeuProLeu	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysBroValLysGlyAsp 263 ::: ::: ::::::	224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	206 IleGInValGInValAsnAspGInThrTyrTyrGInSerPheGInValSerGIu 223 :::	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	536 GTATACATTCAGGATCCCAAAGGAAATCGCATCGCACAATGGCAGAGTTTCCAGTTAGAG 595
Qy 778 ThrGluVall	758 2447	Qy 738 ThrProValo	Oy 718 ThrSerTrp	Qy 698 AspThrAsnl Db 2270 TIGGTGGTG	Qy 681 GlySerSerProHis	Qy 661 AlaGluArg Db 2168 GAGTCAGAT	Qy 652 AspGlyVal' Db 2108 TGTCCACAG	Qy 632 ValPheGln(:::: Db 2048 TTCCTAGAG	Qy 626 PheMetAenSer- ::::: Db 1988 TATATTAATGGAA	620 1928	Qy 601 AlaSerAsnı Db 1868 CCTGATGCTv	Qy 581 ThrGlnPro	Qy 561 LeuTyrTrp	Qy 541 GluIleIle: :::::: Db 1691 GACGTGATT	521 1631	511 1571	1511	Db 1451 TGTGGCCAT
ThrGluValILysValILeILeGluLysSerAspLysPhAAspILeLeuMetThrSerSer /9/		ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717	rProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697 	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	ABPGIYVAITYRASPASNAIAGIUTYR 660	ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651	PheMetAsnSerPheAla 631 ::::: TATATTAATGGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2047	TyrLeuglymet	AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619	ThrGlnProAspSerileValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580 ::	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560 :::::	ProglukenSertrpThrProly861aCy8valilevalTyPrileGlukepAeBoly 540	ACTCATGGACTGCTTGTGAGGAGGAGAGACATGAAGGGCCATTTTCCATCTCAATCCCT 1630	AAAGGGAGGCATTGTCCGAACTGGG	TGTGGCCATACTCAGACAGTCCAGGCACATTATATTCTGAATGGAGGCACCCTGCTGGGG 1510 LeulysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510

LeuGluSer	5 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 ::::: ::::: ::: :::		rgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976	306	ValGln 896 GCTTCT 288 IleArg 916 ::::::	277 277 876	8 Glu
RESULT 7 US-09-880-107-2236 ; Sequence 2236, Application US/09880107 ; Patent No. US20020142981A1 ; GENERAL INFORMATION: ; APPLICANT: Horne, Darci T. APPLICANT: Vockley, Joseph G. APPLICANT: Scherf, Uwe ; APPLICANT: Gene Logic, Inc. ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer ; FILE REFERENCE: 44921-5028-WO ; CURRENT APPLICATION NUMBER: US/09/880,107 ; CURRENT FILING DATE: 2001-06-14	Qy 1349 ValArgasnPheLysValSerAsnTnrGlnAspAlaSerValSerIleValAspTyrTyr 1368	1312 GluAlaIIeSerLeuSerGluThrValLysLysValGluTyrAspHisGly ::::::::::::::::::::::::::::::::::::	Qy 1276 AspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGly 1292	Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258	Qy 1216 SerProLeuAlaValValGln	Qy 1176 G1yG1yPheAlaSerThrG1nAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195	Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle 1142 3602 CAGAAACCCAAGGCACCAGTGGGGCATTTTTACGAACCCCAGGCTCCTCTGCTGAGGTG 3661 Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer 1159

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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2236
LENGTH: 4577
TYPE: DNA
ORGANISM: Homo Sapiens
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 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263
                                                                  TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243
                                                                                                                                                                                                      LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205
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                                   TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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                                                                                  ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly
                                                                                                                     ACTCATGGACTGCTTGTGAAGCAGGAAGACATGAAGGGCCATTTTTCCATCTCAATCCCT
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GCGTCCTCGGTTTAC	GACGTGATTGGGGATTCTGCAAAATATGATGTTGAAAATTGTCTTGGCCAACAAGGTGGAT LeuTyTTxpSerLysValLysAlaGluproSerGluLysValSerLeuArgIleSerVal
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CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US 60/351,885
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR PILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: US 60/362,004
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US-10-331-496A-19
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APPLICANT: HILLAN, KENNETH J
APPLICANT: PHILLIPS, HEIDI S
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
APPLICANT: SPENCER, SUSAN D.
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                   PRIOR
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                                                                                                                                                                                                                                                                                                               APPLICANT:
          OR APPLICATION NUMBER: US 60/345,444
OR FILING DATE: 2002-01-02
OR APPLICATION NUMBER: US 60/351,885
OR FILING DATE: 2002-01-25
OR APPLICATION NUMBER: US 60/360,066
OR FILING DATE: 2002-02-25
OR APPLICATION NUMBER: US 60/362,004
OR FILING DATE: 2002-03-05
OR APPLICATION NUMBER: US 60/366,869
OR APPLICATION NUMBER: US 60/366,869
FILING DATE:
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SMITH, VICTORIA
SPENCER, SUSAN D.
WILLIAMS, P. MICKEY
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2002-03-20
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PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR FILING DATE: 2002-08-21
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NUMBER OF SEQ ID NOS: 95
SEQ ID NO 19
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                   TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle	CTCATCTATGCTGTTTTACCTACCGGG 1690 Qy SlnLeuValPheLysAsnLysIleLys 560	1631 GTGAAGTCAGACATTGCTCCTGTCGCTCGGTTGCTCATCTATGCTGTTTTACCTACC
833 ThrValThrAlaLeuSer		
813 GluaspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle		
798 Glu		
778 ThrGluValLysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797		
758 VallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 		
738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	SerLysSerSerMetAlaValHisSer 458 Qy Db	439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer
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ıj ≽	QyValProGlnSerGlyThrPhe 428	412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe
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າ ດ ≽	luArgArgAsnAsnValValIle 391 AATAAAGTCATA 1195	372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle
H >	371 1147	352 GluphepheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys ::: 1133 CCCTTCTTTGGGCAG
· +j <	spTyrIleIle 351	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle
ט יידו	331 1084	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal
์ฉ—จ	316 1024	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer
ALASETABRABELETRIMETGIUABRIVALHIBGIULEU :::::::::::::::::::::::::::::::::::	988	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp
െ ⊣	276 952	272SerPheTrpGlyLys
561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	Qy 3CTTCCGACTGCCACGGTGAAGATTCA 892 Db	264 ValThrLeuThrPheLeuProLeu
ი	ThrTyrGlyLysProValLysGlyAsp 263 	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp ::: ::: :::::: 773 GAAGAGATGAATGTATCAGTGTGTGGCCTATACACATATGGGAAGCCTGTCCCTGGACAT

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Alignment Scores:

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APPLICANT: Waga, Iwao
APPLICANT: Wanamoto, Jun
APPLICANT: Yanamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Hyperplasia Using Gene Ex
FILE REFERENCE: 44921-5029-US
FULRENT APPLICATION NUMBER: US/09/873,319A
CURRENT APPLICATION NUMBER: US 60/223,323
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
COTTAINED DATE: DOS: 755
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                                                                                                        SOFTWARE: PatentIn Ver.
SEQ ID NO 408
LENGTH: 4577
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Munger, William E. APPLICANT: Kulkarni, Prakash APPLICANT: Getzenberg, Robert
TYPE: DNA
ORCANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134324A1 M11313
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900 GIMMAN		893 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA	272	QY 264 ValThrLeuThrPheLeuProLeu	Qy 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: :::::::::::::::::::::::::::::::::	Qy 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	Qy 206 IleGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::	Qy 186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	Qy 167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 ::: :::	Qy 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166 ::: :::::: Db 476 AAATTTCGTGTTGTCTCCATGGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA 535	Qy 127 LysarglleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146 ::: :::: : :::::	Qy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgVal 106	Qy 72SerValLeuGluAlaGluGlyValPheGluLy8GlySerPheLy8ThrLeuThr 89 :::	Qy 52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71	Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31	-020-095-4 (1-1428) x US-09-873-319-408 (1-4577)	Pred. No.: 3.56e-133 Length: 4577 Score: 1440.00 Matches: 451 Percent Similarity: 46.20% Conservative: 266 Best Local Similarity: 29.06% Matches: 551 Onserv March: 19.60% Tendolo: 551
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Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258 ::::: ::: Db 4016 CAGACCTCCTTGAAATACAATATTT		SerProLeuAlaValValGln	1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro	Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195	Qy 1160 GluGlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175	Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer 1159	Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle 1142		Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLy8AlaLy8GluAla 1107	Qy 1075 LeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088	Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074 ::: Db 3365 GCCCTTCTGGAGATTCCTCTCACAGTCACTCACCCTGTTGTCCGCAATGCCCTGTTTTGC 3424	Qy 1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 ::::: :::: ::: :::	Qy 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallle 1034	Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014	Qy 977 PheGlyABnTyrAspProSerGlySerThrTrpLeuSerAlaPheValieuArg 994	957 MetargGinArgGinArgGinLeuteuTyrGinArgGinAspGiySerPheserAia :::	3005 GATTATCTAAATGAAACACAGCAGCTTACTCCAGAGGTCAAGTCCAAGGCCATTGGCTAT	2945 ATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCTCCTAACATCTATGTACTG

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PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 654
LENGTH: 4577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplast TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 44921-5029-01US CURRENT APPLICATION NUMBER: US/09/960,706 CURRENT FILING DATE: 2001-09-24
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ORGANISM: Homo sapiens
FEATURE:
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   CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal
                                      GTCCCCTCCCTGCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC
                                                                           AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51
                                                                                                                CTCTTGGTCCTCCTGCCCACAGACGCCTCAGTCTCTGGAAAACCGCAGTATATGGTTCTG
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ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle
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                                                                                                                                                                                                        GAAGAAGGAACAGTGGTGGAATTGACTGGAAGGCAGTCCAGTGAAATCACAAGAACCATA
                                                                                                                                                                                                                                         SerProGlyProValGluIleLeuThr------ThrValThrGluSerVal 331
                                                                                                                                                                                                                                                                                    TATGAAATGAAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGCCTCAAGCAATTTTCCTTTTTCCCCTCTCATCAGAGCCCTTCCAGGGCTCCTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATACATTCAGGATCCCAAAGGAAATCGCATCGCACAATGGCAGAGTTTCCAGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leu---IleLyaAspProLyaSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTTCGTGTTTGTCTCCATGGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGACAGTCTGGTCTTTGTCCAGACAGACAAATCAATCTACAAACCAGGGCAGACAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr
                                                                                          GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371
                                                                                                                               ACCAAACTCTCA---TTTGTGAAAGTGGACTCACACTTTCGACAGGGA-----ATT
                                                                                                                                                                ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
                                                                                                                                                                                                                                                                                                                                                                                          LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296
                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTTCCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGGACCAACCCAAGAA-----TTTAAGAAGCGGACCACAGTGATGGTTAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
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                                                                                                                                                                                                                                                                              ----CTTCACACTGAGGCCCAGATCCAA
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LeuLlysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	1148 GTGCGCCTAGTAGATGGGAAAGGCGTCCCTATACCAAATAAAGTCATA 1195 392 ThrValThrGlnArgAanTyrThrGluTyrTrpSerGlySerAanSerGlyAanGlnLy8 411 1196 TTCATCAGAGGAAATGAAAGCAAACTATTACCAATGCTACCACGGATGAG 1246 412 MetGluAlaYalGlnLy8IleAanTyrThrValProGlnSerGlyThrPhe 428 412 MetGluAlaYalGlnLy8IleAanTyrThr
99 798 Glu	Qy 681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697

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                                                                                                                                                                                                                                                                                                          1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258
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                                                                                                                                                                                                                                                                                                                                                                                                             GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGACCTCCTTGAAATACAATATT-----
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LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
                                                                                                                                                     TCTGCCTCCAACATGGCGATCGTTGATGTGAAGATGGTCTCTGGCTTCATTCCCCTGAAG
                                                                                                                                                                                        ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAAACCCAAGGCACCAGTGGGGCATTTTTACGAACCCCAGGCTCCCTCTGCTGAGGTG
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                                                  CCAACAGTGAAAATGCTTGAAAGATCTAACCATGTGAGCCGGACAGAAGTCAGCAGCAAC
                                                                                                  GluAlaIleSerLeu------SerGluThrValLysLysValGluTyrAspHisGly 1328
                                                                                                                                                                                                                                                          GAACCCAAAGCCCACACCAGCTTCCAAATCTCCCTAAGTGTCAGTTACACAGGGAGCCGC
                                                                                                                                                                                                                                                                                                                                                             CCAGAAAAGGAAGAGTTCCCCCTTTGCTTTAGGAGTGCAGACTCTGCCTCAAACTTGTGAT 4102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
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Sequence 3, Application US/10292081A
Publication No. US20030162202A1
GENERAL INFORMATION:
APPLICANT: Kenneth David Becker
APPLICANT: Gonul Velicelebi
APPLICANT: Xin Wang
APPLICANT: Randolph E. Tanzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-292-081A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
SOFTMARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo
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APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380
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  416
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                                                                                                                                                                                                                                                                                                                                        72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
LeuProSerLeuProLeuAsnSerAlaAspGlu------IleTyrGluLeuArgVal 106
-----GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TETTGGTCCTGCCCACAGACGCCTCAGTCTCTGGAAAACCGCAGTATATGGTTCTG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr
                                                                                                  AAAGGACCAACCCAAGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCCCTCCCTGCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC
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                                                                                                                                          ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr
                                                                                                                                                                                                                                                                                           TTCACTGACCTGGAGGGGAGAATGACGTACTCCACTGTGTCGCCCTTC------
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Lars Bertram
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1440.00
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Matches:
Conservative:
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Indels:
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439 SerGluLeuGlnLeuLy8AlaTyrPheLeuGlySerLy8SerSerMetAlaValHi8Ser 458 	LysIleGluPhePro	9	ThrvalThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys ThrvalThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	CCTTCTTTGGGCAG ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351 ::: :::	SerProGlyProValGluIleLeuThrThrValThrGluSerVal	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	ORGANISA SANGRALLIS CHORMAN ARTES AND		111011C11CCAN011IOANGIACAGIGCCAAAGAAAICACAICIIOAAA Ly6HisLeuAsmGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLy8GlyAsp ::::	TyrValleuProLyspheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer ::::		186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisBroIleLeuGlyAspTrpSer 205	TheuIleLysAspProLysSerAspLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166 ::: :::::: 476 AAATTTTCCTCTTTTCATTCAATCAATCAATCACTTTCTAATCACTTTCAATTCACTTTCACTACT
Oy 738 ThrProvalGuLeuGIDALAPREGUE PROPREHELEUASILEUE PROFISES 757	718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuThrThr	Oy 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717 :::	Qy 681 GlySerSerProHis	Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	Qy 652 AspGlyvalTyrAspAsnAlaGlu	Qy 632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651 :::::	Qy 626 PheMetAsnSer	Qy 620 GlyTyr	Qy 601 AlaSerAsnAspIleThrMetGluAsnVallValHisGluLeuGluLeuTyrAsnThr 619 ::::::::: ::: :::	Qy 581 ThrGlnProAspSerIleValGlyIleValAlavalAspLysSerValAsnLeuMetAsn 600	Qy 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	Qy 541 GluileIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560	Qy 521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540	Qy 511LysGlnAsnSerThrMetPheSerLeuThr 520	Qy 493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	Qy 479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	Qy 459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478

2567 GANCANGCGCTCACTCCCTTTTGTGTALACGGCGCAAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCTAACGGCCAAATTC 2653 813 GINASpilalililililililililililililililililili	
Db 3602 CAGAACCCAAGGCACCTTTTACCAACCCCAGCTCCTCTCCTCAAGGTG 361 1413 Gluvalalalalalalalalalalalalalalalalalala	3482 AAAGCACTGCTGGCCTATGCTTTTGCCCTGGCAGGTAACCAGGACAAGAGGAAGGA

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 4577
TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLE
FILE REPERENCE: 37481-323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
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TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer
                                                               IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
                                                                                                                            LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer
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                                                                                                 GGTGGCCTCAAGCAATTTTCTTTTTCCCCTCTCATCAGGGCCCCTTCCAGGGCTCCTACAAG
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813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832	778 ThrGluValLysVallIeIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717 :::	2168 GAGTCAGATGTAÀTĠGGAAGAGGCCATGCACGCCTGĠTĠCATGTTGAAGAG 2218 681 GlySerSerProHisValargLysHisPheProGluThrTrpIleTrpLeu 697		626 PheMetAsnSer	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	1631 GTGAAGTCAGACATTGCTCCTGTCGCTCGGTTGCTCATCTATGCTGTTTTACCTACC
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GAGATGACATCCTATGTGCTCCTCGCTTATCTCACGGCCCAGCCCA	TILL TO THE TENT OF THE TENT O	CTGGAGTCAGCCTGGAAGACAGCACAAGAAGGGGACCATGGCAGCCATGTATATACC LeualaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluala ::		ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallle	977 PheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArg 994		GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu	857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876	842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856

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FILE REFERENCE: 50665-8021 US00
CURRENT APPLICATION NUMBER: US/10/076,816
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
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PRIOR PRILING DATE: 2001-05-02
PRIOR PRILING DATE: 2001-05-02
PRIOR PRILING DATE: 2001-05-06
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PRIOR PILING DATE: 2000-05-02
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NUMBER OF SEO ID NOS: 60
SOPTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 56
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Publication No. US20030056244A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       APPLICANT: Huang, Ning
APPLICANT: Rodiguez, Raymond
APPLICANT: Hagie, Frank E.
TITLE OF INVENTION: Feed Additive Compositions
LENGTH: 4577
TYPE: DNA
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Best Local Similarity:
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                                                                                                                                                                                      IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
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                    CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA
                                                                                                                           ValThrLeuThrPheLeuProLeu---
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                                                                                                                                                               GAAGAGATGAATGTATCAGTGTGTGGCCTATACACATATGGGAAGCCTGTCCCTGGACAT
                                                                                                                                                                                                                                        TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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                                                                                          GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA
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897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg	1811 GCTCCTCAGTCCGGCCCTCCGTGCTGGACCAAAGCGTGCTGCTCATGAAG 1867 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619 Qy
877 LeulysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln ::: ::: 2828GAAGAATTATCCCTGAAACTGCCACCAAATGTGGTAGAAGAATCTGCCCGAGCTTCT	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn
857 GlulysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal
842SeraepalaValThrGlnMetIleLeuValLysalaGluGlyIle	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys
833 ThrValThrAlaLeuSerProThrAla	
813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	Oy 511LysGlnAsnSerThrMetPheSerLeuThr 520
798 GluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510
778 ThrGluValIJ98ValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer	479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492
	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478
ThrP	458 1390
Thrs	429 LysileGluPhePro
	412 MetGluAlaValGinLysileAsnTyrThrValProGinSerGlyThrPhe 428
	392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411 :::
661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	Oy 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391
TGTC	352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371 1133 CCCTTCTTTGGG
	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351 ::
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- 1 } ; ;	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
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                                                                 ACATTTTCCAGCAAATTCCAAGTGGACAACAACAATCGCCTGTTACTGCAGCAGGTCTCA 3955
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------ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
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626 PheMetAsnSerPheAla 631 :::::: 2018 TATATTAATGGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2077	D Q	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331
620 GlyTyrTyrLeuGlyMet 625 [::: 	D Q	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619	Q Q	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp
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541 GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560 :::::	B &	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: :::
521 ProGluAsnSerTrpThrProLysalaCysValIleValTyrTyrIleGluAspAspGly 540	B &	224 TyrValLeuProLyspheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::
511	p Q	206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::
493 LeuLyscluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	B &	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProlleLeuGlyAspTrpSer 205
	95 A	167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 ::: :::
LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	p Q	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166
SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer	B &	127 LysArglleSerValPhelleGlnThrAspLysAlaLeuTyrLysBroLysGlnGluVal 146 :::
429 LysIleGluPhePro	D Q	
412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428	₽ &	90 LeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgVal 106 :::::: :::: ::::: 341GCTGTCCCAAAGTCTTCCATCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 394
392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411	D Q	72SerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThrLeuThr 89 :::
ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle	p Q	52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71
352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371	₽.\$	32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-31CIP
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     LeuAlaValAlaProGly-----
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Tang, Y. Tom
Liu, Chenghua
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Goodrich, Ryle
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Mize, Nancy K
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                                                       976 GAGGCCAATGCCACTCAGAATATCTACATTTCTCCACAAATGGGATCAATGACCTTTGAA 1035
                                                                                                                                                                                               856 ACTGACAAAACAGGATGTTTCTCAGCACCTGTGGACATGGCCACCTTTGACCTCATTGGA
                                                                                                                                                                                                                                     313 LeuAgp------LeuSerSerPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 LeuGlnThrProLeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAla
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AspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTGGTGGCACAGAAGTAGTGGCCACAATCCGGGTGTCGGGA---GTTGGAAATAAC
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                                                                                                                            TATGCGTACAGCCATCAAATCAATATTGTGGCTACTGTTGTGGAGGAAGGGACAGGTGTG
                                                                                                                                                                                                                                                                                                         SerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyr 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAAGACCTTTGGTACTTTCAGTGTGGAGGAATATGTGCTGCCGAAGTTTAAGGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGAATACTCTGGACTGAAGAAGAGGCACTTACATTGTATCTCCTTTCTTGTACCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCTAAATTTCCCC------TCCGTTCAGAAGGTTTGTTTGGACCTGAGCCCT
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                                                                                     SerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePhe
                                                                                                                                                              -----GlyProValGluIleLeuThrThrValThrGluSerValThrGlyIle
                                                                                                                                                                                                                                                                                                                                                                            PheTrpGlyLysLysAspIleThrLysThrPheLysIleAsnGlySerAlaAsnPhe 292
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608 GluAsnValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPhe 626 :::	Val	375 AlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnAvalValIle
Db 2809 GTTCCTGACCCAAGGCTTATGTTACGGTTCTGGGTAAGCAGTTAGAGATTCTTGAC 2868 Qy 902	767 2422 787 2482 2482 807 2524 827 2584 838 2644 851 2704	Qy 636 CysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrTleAspGlyValTyr 655 ::: ::: :::

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1298	1280 ValAspLeuAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeu
4098	4039 TTTAGTCTTAGTGTGGAAATAGGAAAAGCTAGATGTGAGCAACCGACTTCACCTCGATCC
1279	lLys
1263 4038	xArgArgArgArgSerIleGlnAsnGlnGlnAla :: ACAAATATGAAGACC
00	946 GGAATGTACACGTTGGAGGCCTCAGGCCAGGGCTGTGTCTATGTGCAGACGGTGTTGAGA
4 4	. U
1223	1211GlyProSerSerProSerProLeuAlaValValGlnPro
1210 3885	1197 LeuMetAsnThrGluArgThrAsnIleGlnValThrValThr
1196 3825	aAla CACTACCGCC
1178 3765	YPhe
1158 3705	1144 ValAlaAlaTyrAlaLeuLeuSerHi8PheLeuGlnPheGlnThr:::
1143 3645	
1126 3585	1107 AlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSer
1106 3525	1088 ThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLy8AlaLy8Glu
1087 3465	1068 ValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyr
1067 3408	1048 LeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAsp
1047 3348	1028 TrpAspProGlyArgVall1eHisSerGluLeuGlnGlyGlyAsnLysSerProValThr :::
1027 3288	1008 AsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPhe ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
1007 3228	988 LeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAspGln :::
987 3168	968 GlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThrTrp ::: ::
967 3108	948 ASRLeuLySGluLySAlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeuTyr

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1376 ArgSerTyrAsnSerGluValLysLeuSer-SerCysAspLeuCys 1390
4339 AACTTGAAACCAGCAACCATCAAGGTCTATGACTACCTAC
1356 AsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAlaVal 1375
4279 GAGCTCATTAAGAACACTCAGACTTACACCTTCACCATCAGCCAAAGTGTGCTGGTCACC 4338
1336 SerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysValSer 1355
4219 CAGCAACCCCTGGTGAAGAAGGTTGAATTTTGGAACTGACACACTTAACATTTACTTGGAT 4278
-ThrValLysLysValGluTyrAspHisGlyL
4159 GTGGAAGTGAAGATGCTATCTGGGTTCAGTCCCATGGAGGGCACCAATCAGTTACTTCTC 4218
1299 MetGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIleSerLeu 1316
::: ::: ::: 4099 TTGACTCTCACTATTCACACCAGTTATGTGGGGAGCCGTAGCTCTTCCAATATGGCTATT 4158

Search completed: January 17, 2004, 08:49:35 Job time : 1238 secs

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A;Recession: T27828
A;Status: preliminary; translated fr
A;Molecule type: DNA
A;Residues: 1-1508 <WIL-
A;Cross-references: EMBL:Z82090; PII
A;Cross-references: clone ZK337
C;Genetics: A;Gene: CESP:ZK337.1a
A;Map position: 1
A;Introns: 36/2; 116/3; 201/1; 267/2
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090; PIDN:CAB05006.1; GSPDB:GN00019; CESP:ZK337.1a

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•	A;Introns C;Superfa	A; Thirrons: 36/2; 116/3; 201/1; 267/2; 338/3; 413/3; 527/3; 556/3; 691/3; 714/1; 760/2; C; Superfamily: alpha-2-macroglobulin	
•	Query N Best Lo Matches	Query Match 25.2%; Score 1854.5; DB 2; Length 1508; Best Local Similarity 31.8%; Pred. No. 6.3e-97; Matches 476; Conservative 292; Mismatches 562; Indels 169; Gaps 44;	
	Q	15 VCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVL 74	
	В	28 VSTTAAPVKPA-TYMLVAPAVVRPDQPFSVCMNLLKQATDEDMIVRIEVRTERNETIAAR 86	
	S,	75 EAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQD-EILFSNSTRLSFETKRISV 131	
	Дb	87 VISNI-KPGIAQTVSLSEMPAQSLTPRQSYKLYIRGETLNAELIFENENELKYDQKALSV 145	
	Q	132 FIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLGVISK 191	
	DЪ	146 FIQTDRAIYRPASLVRYRAIVVKSDLKPYVGNATIKIFDPSRNLISQTIGVTLDRGVYSG 205	
	Q	192 TFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMNSKHLN 247	
	맑	206 ELQLAEETLIGDWFIEVETSNGVQDKSSFTVDTXVLPKFEVNIKTSSFITIND-DLS 261	
	Ş	248 GTITAKYTYGKPVKGDVTLTF-LPLSFWGKKKNITKTFKINGS 289	
	망	262 VFVDAKYTYGKGVAGKAKVSLELPWHRWHAMVPTIIDENGVKKEEELMVERTVKLNRQGE 321	
	Ø	KNVMDSSNGLSEYLDLSSPGE	
	Дb	322 AAVVFSNDELKRHKLLHEWGGGSIRIVASVTEDITEIERNATHQISTFREEV 373	
	S.	350 IIEFEDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNS 407	
_	Db	374 KLDVEKQGDTFKPGLTYNVVVALKQMDDTPVKATLPKRVQVSTFYNYPYNHDTS 427	

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RPVCLSLYSDVTYQVADQKPANFRLVDYYDPEEQLKMTYAAKQTRSLQEKCG--EDCWP
                                                                                                           CTSFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVK-----KVEYDHGKLNLYLDSVNE
                                                                                                                                                                                                                                   TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQ 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVDGSQKARLDVIGDMMGPVLNNAHKLVQMPYGCGEQNMLNLVPNILVVKYLRATNRNES 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPN
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                                    TOFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRP 1398
                                                                           CCNYTRPGKSNMALAEIDALSGYRFDAEQVHTLTSIEDLQRVEMEKDDTKMNVYFNPLGG
                                                                                                                                                                                             AVNI SANGFGFAI COLNVVYNVKASGSSRRRRS I ONQEAFDLDVAVKENKDDLNHVDLNV
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                                                                                                                                                      AVSINANGTGVVFAQLSYSY-----YRDSLNDDAPFFCSQEIKEIRAG-NRLQLDL
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A;Residues: 1-1519 <WIL>
A;Cross-references: EMBL:Z82090; PIDN:CAB05007.1; GSPDB:GN00019; CESP:ZK337.1b
A;Experimental source: clone ZK337
C;Genetics:
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A;Introns: 36/2; 116/3; 201/1; 267/2; 338/3; 413/3; 527/3; 556/3; 691/3; 714/1; 771/2; C;Superfamily: alpha-2-macroglobulin
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A;Accession: T27829
A;Status: preliminary; translated
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T27829
hypothetical protein ZK337.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T27829
R;White, S.
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RESULT 3

T18544

alpha-2-macroglobulin - Limulus sp.
C;Species: Limulus sp.
C;Species: Limulus sp.
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T18544
R;Iwaki, D.; Kawabata, S.; Miura, Y.; Kato, A.; Armstrong, P.B.; Quigley, J.P.; N
Eur. J. Biochem. 242, 822-831, 1996
A;Title: Molecular cloning of Limulus alpha-2-macroglobulin.
A;Reference number: Z18961; MUID:97175055; PMID:9022715
A;Accession: T18544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1507 <IWA>
A;Cross-references: EMBL:D83196; NID:d1096438; PID:d1020631; PIDN:BAA19844.1
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                                                                                                                                                                                             GEAGGFGGGIRKKINKPVVBIRTYFPETWLWBLQNIGATGELSLKRDIPHTITEWVGSAI
                                                                                                                                                                                                                                                                 STNYLDSITAFDEAGLVVISDMELETRFCKFSGFEDGGRFCPQYDVAFAAPQAANRIGGG
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                                                          QSDKF-----
                                                                                         KSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS-----
                                                                                                                            CISEETGLGVSEA-ATVKGFQPFFVSFTLPYSVIRGEKVPIIVTVFNYLSECLPIKLSLE
                                                                                                                                                                                                                                                                                                 LGMFMNSFAVFQECGLWVLTDANL-----TKDYIDGVYDNAEYAERFMEENEGHIV---
                                                                                                                                                                                                                                                                                                                                 XSVHILSSDNRITEEEVFNKLGGHDYYWPKQATSDYKYCEDYKFKQTEGEHEGSFSSGFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGKGYLKPGLPFYGKLKVEKPDGTPAPGEQ-----IELCRFADRERWNRKRWLEEKIRA
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                                                                                                                                                                                                                               -DIHDFSLG----SSP--HVRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGF
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     - PTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%;
                                                          EMONDTNSYTSCVCGGKSDTTRWMIKPRSLGQVNLTVYGASLPNEAIC
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891

935 838 882

785

823

725

763 673 703 622 643 593

533

524 511 464

584

462 406 357 309

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1476 <IWA>
A;Residues: 1-1476 <IWA>
A;Cross-references: DDBJ:D84338; NID:g1805591; PIDN:BAA12316.1; PID:g1304084
A;Comment: This protein belongs to alpha 2-macroglobulin family.
C;Comment: alpha-2-macroglobulin
C;Superfamily: alpha-2-macroglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
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JC5143
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J. Biochem. 120, 1167-1175, 1996
A; Title: Cloning and sequencing of cDNAs encoding plasma A; Reference number: JC5143; MUID:97164019; PMID:9010766
A; Contents: liver
A; Accession: JC5143
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-macroglobulin precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-dan-1997 #sequence_revision 27-Feb-1997
C;Accession: JC5143
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LSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLN-----ILIKDPKSNLI 176
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                                                                                                                                                                 PVLL----LILLAADASISGKPQYMVLVPSLLHSGTPEKICL-LLTQLNETVTVKASLD
                                                                                                                                                                                                PPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGGKTFWKSPSS--GRYYWGNSIGVEIAGYAVLTLLQHGGASNLAKVTPIIRWLAKQQNY
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                                                                                                                 -LKTASNĻTVSVLEAEGVFEKGSFKTLŢLPSLPLNSADEIYELRVTGRTQDEILFSNSTR
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                        20.3%; Score 1491; DB 2; Length 1476; 28.8%; Pred. No. 2.8e-76; Live 292; Mismatches 524; Indels 300;
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                                                                                                                                         TYTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESI
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Query Match 19.8%; Score 1455; DB 2; Length 1477; Best Local Similarity 29.4%; Pred. No. 3.1e-74; Matches 457; Conservative 237; Mismatches 578; Indels 284; Gaps 50; Qy 13 LCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASN 68 :: : Db 9 LCLFSALLAFLPPASLLNGNSKYMVLVPSQLYTETPEKTCHLLYHLNETVT 59 Qy 69 LTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIFERNTGRTQDEILFSN 118 : : : : : Db 60 VTASLISQRGTRKLFDELVVDKDLFHCVSFTIPRLPSSEEEESLDINIEGAKHKFSE 116 Qy 119 STRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKS 173	y the monomer MID:2472396 cted <sig>atus predicte</sig>	A;Cross-references: GB:J03552; NID:g202571; PIDN:AAAA0628.1; PID:g202572 R;Schweizer, M.; Takabayashi, K.; Geiger, T.; Laux, T.; Biermann, G.; Buhler, J.M.; Gaut Eur. J. Biochem. 164, 375-381, 1987 A;Title: Identification and sequencing of cDNA clones for the rodent negative acute-phase A;Reference number: A27199; MUID:87190405; PMID:2436907 A;Accession: A27199 A;Molecule type: mRNA A;Residues: 1253-1477 <sch> A;Cross-references: GB:M28297; NID:g204930; PIDN:AAA63493.1; PID:g204931 A;Experimental source: liver, Clone pIJCDNA6 A;Experimental source: liver, Clone pIJCDNA6 A;Engchild, J.J.; Salvesen, G.; Thogersen, I.B.; Pizzo, S.V.</sch>	RESULT 5 A29952 A29952 alpha-1 proteinase inhibitor III precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Decies: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999 C;Accession: A29952; A27199; A34278 C;Accession: A29952; A27199; A34278 R;Braciak, T.A.; Northemann, W.; Hudson, G.O.; Shiels, B.R.; Gehring, M.R.; Fey, G.H. J. Blol. Chem. 263, 3999-4012, 1988 A;Title: Sequence and acute phase regulation of rat alpha-1-inhibitor III messenger RNA. A;Reference number: A92709; MUID:88153707; PMID:2831216 A;Accession: A29952 A;Molecule type: mRNA A;Residues: 1-1477 < GRA>		1126 SSES 1187 RPQN 1171 QRNS 1171 QRNS 1243 QQNS 1221 VQPM 1257 SIQN 1362 SPQ- 1362 SPQ-
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A; Molecule type: DNA
A; Molecule type: DNA
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A; Residues: 672-747 < MAR>
R; Matthijs, G.; Devriendt, K.; Cassiman, J.J.; Van Den Berghe,
R; Matthijs, G.; Devriendt, K.; Cassiman, J.J.; Van Den Berghe,
B; Mochem. Biophys. Res. Commun. 184, 596-603, 1992
B; Title: Structure of the human alpha-2 macroglobulin gene and
A; Title: Structure of the human alpha-2 macroglobulin gene and
                                                                                                                 A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-29 <AMAT'> A;Residues: 1-29 <AMAT'> A;Sottrup-Jensen, L.; Stepanik, T.M.; Kristensen, T.; Wier: 0, 1001. Chem. 259, 8318-8327, 1984
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                       A;Accession: A92486
A;Molecule type: pro
A;Residues: 24-562,
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A;Title: Human alpha 2-macroglobulin gene is located on A;Reference number: I39375; MUID:85219061; PMID:2408344
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C;Date: 05-Apr-1983 #sequence revision 30-Jun-1987 #text change 08-Dec-2000
C;Date: 05-Apr-1983 #s9375; S09107; JN0262; A92486; S66634; A01256
C;Accession: A94033; I39375; S09107; JN0262; A92486; S66634; A01256
R;Kan, C.C.; Solomon, B.; Belt, K.T.; Chain, A.C.; Hiorns, L.R.; Fey, G.
Proc. Natl. Acad. Sci. U.S.A. 82, 2282-2286, 1985
A;Title: Nucleotide sequence of cDNA encoding human alpha-2-macroglobulin and A;Reference number: A94033; MUID:85190481; PMID:2581245
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A;Accession: JN0262
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A;Residues: 832-999,'I',1001-1147,'D',1149-1194,'D',1196-1474 <BEL>
A;Cross-references: GB:M36501; NID:g177871; PIDN:AAA51552.1; PID:g177872
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A; Residues: 1-1474 <KAN>
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A;Note: hydrolysis of the thiolester bond during amino acid sequencing o
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:Molecule type: protein
:Residues: 24-562,'E',564-974,'Z',976-999,'I',1001-1474 <SOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A genetic polymorphism in a functional domain of
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                                                                                                                                                                                                                 D.M.; Jones,
                                                                                                                                                     complete
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KRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQWLSQQSD

185

FTDLEAENDVLHCVAF-----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN 124

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186

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A; Molecule type: protein
A; Residues: 1337-1343 cDCl>
A; Residues: 1337-1343 cDCl>
C; Comment: This inhibitor is able to inhibit all four classes (EC 3.4.21-3.4.24) of endog stertiary conformation, entrapping the proteinase. This results in hydrolysis of its this e and appears to unmask a receptor-specific binding site.
C; Comment: The entrapped enzyme remains active against low molecular weight substrates (EC; Comment: The wide specificity of this inhibitor is attributed to the primary sequence (c); Comment: The wide specificity of this inhibitor is attributed to the primary sequence (c); this of a variety of plasma proteinases, form primary (residues 704-809) and secondary (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-1474/Product: alpha-2-macroglobin #status experimental <MA2>
F;693-694,704-709,719-723,730-735/Region: inhibitory #status predicted
F;698-742/Region: bait region
F;698-742/Region: bait region
F;698-742/Region: bait region
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-287,289-28
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A;Map position: 12p13.3-12p12.3
C;Complex: homotetramer; dimer of disulfide linked dimers
C;Superfamily: alpha-2-macroglobulin
C;Keywords: glycoprotein; plasma; proteinsse inhibitor; thiolester
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R;Hall, P.K.; Nelles, L.P.; Travis, J.; Roberts, R.C.
B;chem. Biophys. Res. Commun. 100, 8-16, 1981
B;Cchem. Biophys. Res. Commun. 100, 8-16, 1981
A;Title: Proteolytic Cleavage sites on alpha-2-macroglobulin resulting in
A;Reference number: A90099; MUID:81255805; PMID:6167263
A;Contents: annotation; inhibitory site
A;Ronttensen, S.B.; Sottrup-Jensen, L.; Hansen, H.F.; Petersen, T.E.; Magnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Virca, G.D.; Salvesen, G.S.; Travis, J.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1297-1302, 1983
A;Tile: Human neutrophil elastase and cathepsin G clea-
A;Reference number: A91713; MUID:84030513; PMID:6195065
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                     451;
                   -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET
                                                                                                                                                                                                 LLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTV
                                                                                                                  LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
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167-173, 1981
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Pred. No. 2.
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2.2e-73;
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453 SMAVHSLEKSPSKIYIQLKIKDENIKVSS-PERLVVSGNKKIKE 495	05 GNAAPPGŚQHHTGADGTFTFTI-DTGDFNRSDTIFLEATDPEFNSTAHPSVTYQQ 45	CTESSET	336 RNVSTNVPFKQHDYIIEFFDYTTVLKPSLNÉTATVKVTRADGNQLTLEERRNNVVITVTQ 395 	291 NFSFNDEEMKNVMDSSNGLSEY-LDLSSPGPVEILTTVTESVTGIS 335 : : : : : : : : :	231 VTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSA 290 :: :	174 NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFE 230	115 LFSNSTRLSFETKRISVFIQTDKALYKÞKQEVKFRIVTLFSDFKP-YKTSLNILIKDÞKS 173 :	66 ASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEI 114	10 AHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKT 65	/ Match 19.4%; Score 1424; DB 2; Length 1503; Local Similarity 28.3%; Pred. No. 1.8e-72; Lecal Similarity 28.3%; Pred. No. 1.8e-72; Les 442; Conservative 256; Mismatches 600; Indels 266; Gaps 48;	RESULT 7 743166 alpha-2-macroglobulin - Japanese lamprey C;Species: Lampetra japonica (Japanese lamprey) C;Acces: Lampetra japonica (Japanese lamprey) C;Accession: T43166 R;Nonaka, M. Submitted to the EMBL Data Library, November 1992 A;Reference number: Z22323 A;Reference number; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1503 <non> A;Residues: 1-1503 <non> A;References: EMBL.D13567; PIDN:BAA02762.1 A;Experimental source: liver; clone Cl.3 and Cl1.10 C;Superfamily: alpha-2-macroglobulin</non></non>	1329 KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS 1380 	1276 DLN-HVDLNVCTSFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVKKVEYDHG 1328 :	1223PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKD 1275	1176 GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGFSSPSPLAVVQ 1222 : : :

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                                                                                     YDFVKKVEVDASRVVIYLDKVDKKPIAIKLSVTQDIAVDNLQPATVRVYDYYATEDAATS
                                                                                                                                                                                                                               DLDVAVKE----NKDDLNHVDLNVCTSFSGP-GRSGMALMEVNLLSGFMVPSEAISLSET-
                                                                                                                                                                                                                                                                                                                                                                                                                            QRNSLGGFASTQDTTVALKALSEFAAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --FLESEFSRGISDNYTLALITYALS-SVGSPKAKEALNMLTWRAEQEGGMQFWVSSESK
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                                            SYNS 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLXGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLSAESIFQRLQVQDLTYYDYGIERWDCSPEHYRRKRSYGVWMDDFQNSVHRLFKGMGL
                                                                                                                                    ---VKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVR
                                                                                                                                                                                     SLSVETNPANCSKAARKGFQINVEVSYHGERGESNMALVEVKMISGYSAVKSSLKELQTF
                                                                                                                                                                                                                                                                             NALILHQVQLPPPVPAPMVSSCTVEATGQGCALFQVSLKYNEPPKSSKPK-----F
                                                                                                                                                                                                                                                                                                                              SS-----PSPLAVVQPMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDKDEEDBEGGFNFRRSYGGTTSAAVETTAYALLSRLAVPGQLAASATSSNIGVVQWLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVLES-----SNAHLLALASYAFSLSADGATAQALRDALQSRAVTKGGLTHWQEANKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQRQLTYKRDDHSYSAFGKSDDDGNTWLTAFVLKSFVRASKHIAVSEDHITGPFSWLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDIMGSALQNLDKLLTLPTGCGEQNMVKFAPNIYIQEYLQNSGQLTDAVRDKALNFLRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVDTVVRSVIVEPEGIPKELAYSSL--LCPKSPASERFVFNLPLPANVIVGSARAYATIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITAI
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                                                                                                                                                                                                                                                                                                                                                                             QRNAYGGFSSTQDTVVGLQALSAFAALIDGDGGGGGSGGIKAVVLDSAHTLLREVSIDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - AAGGPRGAASCVCPDRKG-LFSFLIEPLALGTVNVSVRAAAVHSDEPCGNEVVVVPEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SIRVFTPFFVEPVLPYSVVRGETPPLAISVHNYLHSCLKIEVTLLDSEHFAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PHVRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVLTDTTV-KRSVDCHQLMHRHRIAYSMETVASPGLRFSDRG-----NISPVGQGGAMF
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1497
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RESULT 8
$15904

alpha-l proteinase inhibitor III, variant 1 precursor - rat
alpha-l proteinase inhibitor III, variant 1 precursor - rat
C;Species; Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 16-Jul-1999
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 16-Jul-1999
C;Accession: $15904; $52235; $29737; B34278; B29952; C29952; B27199
C;Accession: $15904; $52235; $29737; B34278; B29952; C29952; B27199
C;Accession: $15904; $52235; $29737; B34278; B29952; C29952; B27199
A;Introne: 29/2; yu/3; x=x,2
C;Superfamily: alpha-2-macroglobulin
C;Keywords: proteinase inhibitor; thiolester bond
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1487/Product: alpha-1 inhibitor III variant 1 #status predicted <MAT>
F;648-723/Region: bait region #status predicted
F;648-723/Region: bait region #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 684-715,'N','11-733 <ENG>
A;Residues: 684-715,'N','11-733 <ENG>
R;Braciak, T.A.; Northemann, W.; Hudson, G.O.; Shiels, B.R.; Gehring,
A; Biol. Chem. 263, 3999-4012, 1988
A;Title: Sequence and acute phase regulation of rat alpha-1-inhibitor
A;Reference number: A92709; MUID:88153707; PMID:2831216
A;Accession: B29952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Thomsen, N.K.; Sottrup-Jensen, L. Arch. Biochem. Biophys. 300, 327-334, 1993
A;Title: alpha-macroglobulin domain structure studied by A;Reference number: S29737; MUID:93143334; PMID:7678727
A;Accession: S29737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Schweizer, M.; Takabayashi, K.; Geiger, T.; Laux, T.; Bierma
Eur. J. Biochem. 164, 375-381, 1987
A;Tille: Identification and sequencing of cDNA clones for the
A;Reference number: A27199; MUID:87190405; PMID:2436907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 315-409;1064-1079,'LAASGAPDHC',1090,'TMP'
A;Cross-references: GB:M22361; GB:M22362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 80-262, 269-361 <BR2>
A; Cross-references: GB: M22360; NID: g202583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-3,'D',5-86,'V',88-136,'M',138-169,361-364,'M',366,'V',368-397,'H',
A;Cross-references: GB:J03552; GB:M22359
A;Note: the authors translated the codon ATG for residue 174 as Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 25-32,776-280, 'XG',314-320, 'X',322, 'SL',717, 'VVAV',722-726,'Q',728,1205-1218
R;Enghild, J.J.; Salvesen, G.; Thogersen, I.B.; Pizzo, S.V.
J. Biol. Chem. 264, 11428-11435, 1989
J. Biol. Chem. 264, 11428-11435, 1989
A;Title: Proteinase binding and inhibition by the monomeric alpha-macroglobulin rat alpha
A;Reference number: A34278
A;Accession: B34278
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A;Residues: 1-1487 <REG>
A;Cross-references: EMBL:X52984; NID:g55561;
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FEBS Lett. 282, 368-372, 1991
A;Title: Differential regulation of the two mRNA species
A;Reference number: S15904; MUID:91243832; PMID:1709877
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1416-1483,'N',1485-1487
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A; Residues: 1-161 <SIC>
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                                                                                                                                                                                                                                                                                                                             A; Experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B27199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.; Laux, T.; Biermann, G.; Buhler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAA40633.1; PID:g554402
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491 KRLKELSYMVVSRQQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIED 538 A26122 488 LPQIVFYLVMAQGSILQTGNHTHQVEPGVSQVQGNFALEIFVEESMYPVAKMLIYTILP 547 A26122 A1pha-2 A26122 A26	MARCHES 454; CORRESTVALIVE 24; MISHRICHES 57; Indels 290; Gaps 55; 13 LCVCTAALAVAPGPRELVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASN 68 : :
RESULT 9 A26122 alpha-2-macroglobulin precursor [validated] - rat A26122 Alpha-2-macroglobulin precursor [validated] - rat A26122 Alpha-2-macroglobulin precursor [validated] - rat A26122-macroglobulin precursor [validated] - rat A26122-macroglobulin precursor C; Paccession: A2612; A05278; S03431; S33843; A256414; I52403; I54013 C; Paccession: A26122; A05278; S03431; S33843; A256414; I52403 C; Paccession: A26122; M05278; S03431; S33843; A256414; I52403 C; Paccession: A26122; M05278; M05278; PMID:2432068 A; Paccession: A26122; M05278; M05278; PMID:2432068 A; Paccession: A26122; M05278; M05278; PMID:2432068 A; Paccession: A26122; M05278; N1D:2502591; PIDN:AAA40636.1; PID:2502592 A; Polecule type: mRNA A; Pacsidues: 1-1472 < GEH5 A; Complementary to rat alpha-2macroglobulin mRNA. A; Pacsidues: 1-1472 < GEH5 A; Polecule type: mRNA A; Pacsidues: 1-16-227; 420-489; L',491-526 < HAY> A; Pacsidues: 176-227; 420-489; L',491-526 < HAY> A; Paccession: S03431 A; Paccessi	957 ARAHFSYMGDILSSAIKNTQNLIQMPYGCGEQNNVLFAANIYVLKYLNETQQLTEKIKSK 1016 953 ALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTHLSAFVLRCFLEADPXIDIDQNVL 1010 :

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A;Title: Sequence analysis of the putative regulatory region of rat alpha-2-macroglobul
A;Reference number: 154013; MUID:88112864; PMID:2448189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the authors translated the codon ATT for residue 38 as Thr R;Northemann, W.; Shiels, B.R.; Braciak, T.A.; Hanson, R.W.; Heinrich, P.C.; Fey, G.H. Biochemistry 27, 9194-9203, 1984-92003 of the rat alpha 2-macroglobulin gene. A;Title: Structure and acute-phase regulation of the rat alpha 2-macroglobulin gene. A;Reference number: 152403; MUID:89207509; PMID:2468362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S33843; MUID:93307297; PMID:7686489
A;Accession: S33843
A;Molecule type: protein
A;Residues: 28-40, 'R', 42-48 <WAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23,74,25-227 <RE2>
A;Cross-references: GB:M22670; NID:g205388; PIDN:AAA41592.1; PID:g205390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-146 <RES>
A;Cross-references: GB:M23567; NID:g202598; PIDN:AAA77658.1; PID:g554404
R;Tsuchiya, Y.; Hattori, M.; Hayashida, K.; Ishibashi, H.; Okubo, H.; Sakaki,
Gene 57, 73-80, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Northemann, W.; Heisig, M.; Kunz, D.; Heinrich, P.C.
J. Biol. Chem. 260, 620-6205, 1985
A;Title: Molecular cloning of cDNA.sequences for rat alpha-2-macroglobulin and measureme
A;Reference number: A22614; MUID:85207604; PMID:2581948
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Best Local S
Matches 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond;1-27/Domain: signal sequence #status predicted <SIG>;28-1472/Product: alpha-2-macroglobulin #status experimental <WAT>
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384
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                                                                                                                                                                                                                                                                                                                                                                                                  121 RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426;
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                                TQRNYTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILED---SSELQLKAYF---
                                                                                                                                    CFSQLVKTKSFQLK-RQEYEMQLDVHAKIQEEGTGVEE----TGKG----LTKITRTITK
                                                                                                                                                                                                                    CSMNSKHLNGTITAKYTYGKPVKGDVTLTFL-----PLSFWGKKKNI-------
                                                                                                                                                                                                                                                                                          QNFNLEGGLKQLSFPLSSEPTQGSYKVVIRTESGRTVEHPFSVEBFVLPKFEVRVTVPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TASN--LTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEI--YELRVTGRTQDEILFSNST 120
                                                                                                                                                                                                                                                                                                                                                                  TVLVKKKESLVFAQTDKPIYKPGQTVRFRVVSLDESFHPLNELIPLLYIQDPKNNRIAQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLLLRLLLLLPTDASA-PQKPIYMVMVPSLLH-AGTPEKACFLFSHLNETVAVRVSLES 70
                                                                                                      ISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLITAAHLICVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLK 64
----YETIFIGAD-----EANLYINTTTDKHGLAR--FSINTDDIMGTSLTVRAKYKDS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                              TKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTG 333-
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1334 1417	DLNVCTSFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVKKVEYDHGKLNLYL::: :::::::::::::::::::::::::::::::	1281 1358
1280 1357	AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHV	1225 1309
1224 1308	TQDTTVALKALSEF-AALMVTERTNIQVTVTGPSSPSPLAVVQPM	1181 1249
1180 1248	woprsldievaayallshflofqtsegipimrwlsrornslogfas 	1135 1193
1134 1192	SRGISDNYTLALITYALSSVGSPKA-KEALNMLTWRAEQEGGMQFWVSSESKLSDS	1080 1134
1079 1133	SNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEF	1023 1074
1022 1073	YQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQK 	967 1016
966	SINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELL:	907 956
906	KAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSPPPNTVTGSERVQITAIGDVLGP	852 904
851 903	LLVPSEDGATVLFPIRFTHLGEIPITVTALSPTASDAVTQMILV	808 845
807	FFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSSEINATGHQQT : : :-!: 	748 790
747 789	KHPPETWIWLDINMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQP: : : : : :	688 731
687 730	-FAVFQECGLWVLTDANLTKDYI-DGVYDNAEYAERFMEENEGHIVDIHDFSLGSSPHVR : : : : : : : : :	630 671
629 670	NASNDITMENVVHELELYNTGYYLGMFMNS ::: ::: ::: ::: ::: ::: ::: ::: ::	600
599	GEIISDULKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLM 	540 552
539 551	RLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDD	492 492
491 491	LGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNK :	448 432

Qy 496 LSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDGE 541	Qy 290 ANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVST 340 I : : : : :	Qy 13 LCVCTAALAVAPGPRFLUTAPGIIRPGGNUTIGVELLEHCPSQUTVKAELLKT 65	RESULT 10 B41185 alpha-2 macroglobulin homolog MUG2 - mouse C;Species: Mus musculus (house mouse) C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-Jul-1999 C;Accession: B41185 R;Overbergh, L., Torrekens, S.; Van Leuven, F.; Van den Berghe, H. J. B101. Chem. 266, 16903-16910, 1991 A;Title: Molecular characterization of the murinoglobulins. A;Reference number: A41185; MUID:91358495; PMID:1840592 A;Accession: B41185 A;Reference type: mRNA A;Residues: 1-1451 <ove> A;Cross-references: GB:M65238; NID:919888; PIDN:AAA73041.1; PID:9199889 C;Superfamily: alpha-2-macroglobulin Ouery Match D19.1%; Score 1402; DB 2; Length 1451; Best Local Similarity 27.7%; Pred. No. 3.1e-71; Matches 439; Conservative 250; Mismatches 527; Indels 370; Gaps 54;</ove>
RESULT 11 \$13495 \$13495 \$13495 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 16-Jul-1999 C;Accession: \$13495; \$09106; A34230; PS0077; \$21637 R;Devriendt, K.; van den Berghe, H.; Cassiman, J.J.; Marynen, P. Biochim. Biophys. Acta 1088, 95-103, 1991 A;Title: Primary structure of pregnancy zone protein. Molecular cloning of a full-length A;Reference number: \$13495; MUID:91113734; PMID:1989698 A;Accession: \$13495 A;Status: not compared with conceptual translation A;Residues: 1-1482 cDEV> A;Cross-references: EMBL:X54380; NID:935824; PIDN:CAA38255.1; PID:935825 R;Marynen, P.; Devriendt, K.; van den Berghe, H.; Cassiman, J.J.	52 52 53 63 17	929 PAPNIYILDKITKKKOLTDNIKEKALSFMROGYORELLYQREDGSFSAFGNYDPSGST	Qy 680

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A;Map position: 12p13-12p12.2
A;Introns: 73/3; 116/2; 146/3; 169/3; 703/1;
A;Note: the list of introns may be incomplete
C;Superfamily: alpha-2-macroglobulin
F;685-735/Region: bait region
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A;Molecule type: protein
A;Residues: 670-752,'Q',754-759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sottrup-Jensen, L.; Sand, O.; Kristensen, L.; Fey, G.H.
J. Biol. Chem. 264, 15781-15789, 1999
A;Title: The alpha-macroglobulin bait region. Sequence diversity and localization of A;Reference number: A34230; MUID:89380162; PMID:2476433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 668-690, 'M', 692-753 <MAR>
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A;Title: A genetic polymorphism in a functional domain of human pregnancy zone
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                                                  QSPPASHAHLQVAAA-PQSLCALRAVDQSVLLMKPEAELSVSSVYNLLTVKDLTNFPDNV
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RESULT 12

A41185

A41186

alpha-2 macroglobulin MUG1 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-#
C; Accession: A41185
R; Overbergh, L; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A; Title: Molecular characterization of the murinoglobulins.
A; Reference number: A41185; MUID:91358495; PMID:1840592
A; Accession: A41185
A; Status: preliminary
A; Molecule type: mRNA
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12-Apr-1995

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A;Residues: 1-1476 <OVE>
A;Cross-references: GB:M65736
C;Superfamily: alpha-2-macroglobulin
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                                                                  SVQLEASPDFTAVPVGDD-----QDSYCLSANGRHTSSWLVTPKSLGNVNFSVSAEAQQ
                                                                                                                              KVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPT
                                                                                                                                                                                                                                                                                                                      RTTLSKRPEEPPRKDPSSNDPLTETIRKYFPETWVWDIVTVNSTGLAEVEMTVPDTITEW
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            -DAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSF
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A;Molecule type: mRNA
A;Residues: 20-1473 <RII2>
A;Cross references: EMBL:X78801; NID:g671863; PIDN:CAA55385.1.
A;Cross references: EMBL:X78801; NID:g671863; PIDN:CAA55385.1.
A;Cross references: EMBL:X78801; NID:g671863; PIDN:CAA55385.1.
A;Nielsen, K.L.; Sottrup-Jensen, L.
Biochim. Biophys. Acta 1162, 230-232, 1993
A;Title: Evidence from sequence analysis that hen egg-white ov A;Reference number: S29836; MUID:93192299; PMID:7680577
A;Reference number: S29836
A;Molecule type: protein
A;Residues: 977-980, W',981-1007, M',1009, K',1010-1028 <NI3>
A;Rolecule type: protein
A;Residues: 977-980, W',981-1007, M',1009, K',1010-1028 <NI3>
A;Rolecule type: protein
A;Residues: 977-980, W',981-1007, M',1009, K',1010-1028 <NI3>
A;Rolecule type: protein
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C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1987 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
C;Accession: 150671; 150672; $29836; A20872; A33715
R;Nielsen, K.L.; Sottrup-Jensen, L.; Nagase, H.; Thogersen, H.C.; Etzerodt, DNA Seq. 5, 111-119, 1994
A;Title: Amino acid sequence of hen ovomacroglobulin (ovostatin) deduced from A;Reference number: 150671; MUID:95218210; PMID:7535598
A;Accession: 150671
                                                                                                                                                                                                                                                                                                                                               A;Status: translated from
                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I50672
                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: X78801; NID: g671863;
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A; Residues: 1-1473 < NIE>
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J. Biol. Chem. 264, 8779-8785, 1989
A;Title: Interaction of human rheumatoid synovial collagenase (matrix metalloproteinase kinetics and identification of matrix metalloproteinase cleavage sites.
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A;Residues: 37-49 <NAG>
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A; Molecule type: mRNA
A; Residues: 1-1500 <a href="https://www.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.nc.gov.n
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R;Warmegard, B.; Martin, N.; Johansson,
Biochemistry 31, 2346-2352, 1992
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alpha-1-macroglobulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
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A;Molecule type: protein
A;Residues: 25-29, 'F',31-44 <LONs
A;Residues: 25-29, 'F',31-44 <LONs
C;Superfamily: alpha-2-macroglobulin
C;Keywords: glycoprotein; plasma; proteinase inhibitor
C;Keywords: signal sequence #status predicted <SIGs
F;1-24/Domain: signal sequence #status predicted
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                                                                                                                                                          TRVHKPRYCPMYQAYPPLPYVGEPQALAMSAIPGAGY-----RSSNIRTSSMMMGAS
                                                                                                                                                                                                                                                      L-ELYNTGYYLGMF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MAVHSLFK--SPSKTYIQLKTRDENIKVGSPFELVV-----SGNKRLKELS--YMVVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T--NFTFSFMG------
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TSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTA---LSP--
                                                           LTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILM
                                                                                                            ----PHVRKHFPETWIMLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLG
                                                                                                                                                                                                                   LPQKAEQGAYLGPLPYKGGENCIKAEDITHNGIVYTPKQDLNDNDAYSVFQSIGLKIFTN
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                               LSST-ISHKVFQPFFLELTLPYSVVRGEAFILKATVLNYMPHCIRIHVSLEMSPDFLAVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMR 958
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                                               RTEVNTNHVLIYIEKLTNQTMGFSFAVEQDIPVKNLKPAPVKVYDYYETDEFAIEEYSA 1489
                                                                              KVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS 1380
                                                                                                               TLPLNFDKAEHHRKFQIHINVSYIGERPNSNMVIVDVKMVSGFIPVKPSVKKLQDQSNIQ
                                                                                                                                            AVKENKODLNH----VDLNVCTSFSGP-GRSGMALMEVNILLSGF--MVPS-EAISLSETVK
                                                                                                                                                                              NRLLLQEVRLADLPGNYITKVSGSGCVYLQTSLKYNILPEA--
                                                                                                                                                                                                                                               KOONSHGGFSSTODTVVALQALSKYGAATFT-KSNKEVSVTIESSGT---VSGTLHVNNG
                                                                                                                                                                                                                                                                              RORNSLGGFASTODTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVOPMAVN--
                                                                                                                                                                                                                                                                                                                VEENVREMRSFSYKPRAPSAEVEMTAYVLLAYLTSASSRPTRDLSSSDLTTASKIVKWIS
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A; Molecule type: mRNA
A; Residues: 1-1464 < IWA>
A; Cross-references: DDBJ:DB4339
C; Superfamily: alpha-2-ma------S 밁 Ş C;Superfamily: alpha-2-macroglobulin F;1-23/Domain: signal sequence #status A; Accession: JC5144 A; Status: preliminary A; Reference number: JC5143; A; Contents: liver A;Title: Cloning and sequencing of cDNAs er A;Reference number: JC5143; MUID:97164019; R;Iwasaki, H.; Suzuki, Y.; Sinohara, J. Biochem. 120, 1167-1175, 1996 Query Match Local Similarity 16 73 13 VLEA--LALLMTAASVHKKPQYMVLVP-LCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVS 18.7%; ilarity 27.9%; Conservative 24: 243; -EGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNS Score 1374.5; DB 2; Pred. No. 1.1e-69; 3; Mismatches 596; predicted <SIG> encoding plasma 9; PMID:9010766 ----TQLYTEVPEKSCLHLHYLKETVTVSAS Indels Length 1464; alpha-macroglobulin 271; Gaps 63 72 and murinog

murinoglobulin precursor - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 31-Jan-1997 #sequence_revision

27-Feb-1997

#text_change

17-Mar-1999

C; Accession: JC5144

1085 1134	1033 VIHSELQGGNKSPYTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISD : :: :	
1032 1076	975 SAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGR : : : :	
974 1016	915 IRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSF 	
914 956	855 GIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASL 	
854 899	812 SEDG-ATVLFPIRPTHLGEIPITVTALSPTAS	
811 839	752 LNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSSEINATGHQQTLLVF 	
751 786	692 ETWIWLDTNMGYRIYQEFEVTVÞDSITSWVATGFVISEDLGLGLTTTTÞVELQAFQÞFFIF	
691 727	640 VLTDANLTKDYIDGVYDNAEYAERFMEENEGHIVDIHDFSLGSSPHVRKHFF	
639 677	06 TMENVVHELEL	
605 617	YWSKVKAEPSE : ;; SFRPAQSLPAS	
545 558	498YMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISD	
497 498	田・ ス	
443 450	394 TORNYTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFFILEDSSELQL	
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335 345	296DEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGIS	
295 285)VTLTFLPLSFWGKKKNITKTFKINGSANFSFN 	
237 237	179 WLSQQSDLGVISKTFQLSSHPILGDWSIQV-QVNDQTYYQSFQVSEYVLPKFEVTLQTPL	
178 177	120 TRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKP-YKTSLNILIKDPKSNLIQQ : :	
117	EVHEDLFQCVSFTLPRTSSPNEVAFLSVQIKGRTHTFSEE	

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ALIGNMENTS

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EMBL; J03552; AAA40628.1; EMBL; M22558; AAA40629.1; PIR; A29952; A29952. HSSP; P01023; 1BV8. GO; GO:0017114; F:wide-spectr InterPro; IPR002890; A2M N. InterPro; IPR002599; A2M N. InterPro; IPR00477; ALPHA_2 MAC Serine procease inhibitor; G1 Liver; Thioester bond. SIGNAL 1 24 CHAIN 25 1477 DOMAIN 601 750 DISULFID 48 86 DISULFID 251 295 DISULFID 269 283 DISULFID 269 283 DISULFID 269 283	"Sequence and acute phase re messenger RNA."; J. Biol. Chem. 263:3999-4012 -!- FUNCTION: PROTEBASE INHIB TARGETS, WHICH ATTACHES -!- SUBUNIT: MONOMER: -!- MISCELLANISOUS: THIS INHI ACUTE PHASE!- SIMILARITY: TO OTHER PRO INCLUDING COMPLEMENT COM This SWISS-PROT entry is cop between the Swiss Institute the European Bioinformatics use by non-profit institute entities requires a license or send an email to licensee or send an email to licensee	SULT 1 Alia RAT P14046; 01-APR-1990 (Rel. 14, Lest seq land) 01-APR-1990 (Rel. 14, Last seq land) 15-SEP-2003 (Rel. 42, Last ann land) 15-SEP-2003 (Rel. 16, Last ann land) 16-SEP-2003 (Rel. 16, Last ann land) 18-SEP-2003 (Rel. 14, Las
inhibitor activity; NAS 1. Plasma; Bait region; Si IBITOR III. (APPROXIMATELY). TY. TY. TY.	hase regulation of rat alpha 1-inhibitor III 199-4012(1988). B INHIBITOR WITH A WIDE SPECTRUM OF PROTEIN IIS INHIBITOR HAS REDUCED PLASMA CONCENTRATIONS IN IIS INHIBITOR HAS REDUCED PLASMA CONCENTRATIONS IN HER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY, HENT COMPONENTS C3, C4, AND C5. HENT COMPONENTS C3, C4, AND C5. There are no restrictions on its institute of Bioinformatics and the EMBL outstation stitute of Bioinformatics and the EMBL outstation stitute of Bioinformatics and the MBL outstation stitute of Bioinformatics and t	PRT; 1477 AA. reated) ist sequence update) ist annotation update) recursor. data; Craniata; Vertebrata; Euteleostomi; intia; Sciurognathi; Muridae; Murinae; Rattus. PARTIAL SEQUENCE. 1-2831216; 1-0., Hudson G.O., Shiels B.R., Gehring M.R.,

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Similarity
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RESULT 2
A2MG HUMAN
ID 7A2MG HUMAN STANDARD; PRT; 1474 AA.
ID 7A2MG HUMAN STANDARD; PRT; 1474 AA.
AC P01073; Q13677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin precursor (Alpha-2-M).
GN A2M.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrhini; Homini
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aureus V-8 proteinase.";
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ottrup-Jensen L.,
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GO; GO:0016975; F:alpha-2 macroglobulin;
InterPro; IPR002890; A2M N.
InterPro; IPR001599; MacroglobinA2.
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Hum. Genet. 88:313-319(1992).
-i- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY
-I- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY
-INTUMIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH
CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
CALLED THE 'BAIT REGION' WHICH A PROTEINASE CLEAVES THE BAIT
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EMBL; Z11711; CAA77774.1; --
EMBL; M36501; AAA51552.1; --
EMBL; X68728; CAAA46670.1; --
EMBL; X68729; CAAA4670.1; JO:
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Genew; HGNC:7; A2M.
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"Cloning of the human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91187639; PubMed=1707161;
Poller W., Faber J.-P., Olek K.;
"Sequence polymorphism in the human alpha2-macroglobulin
Nucleic Acids Res. 19:198-198(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macroglobulin.";
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                                              3D-structure;
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MEDLINE=92128897; PubMed=1370808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A COMPORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPED BUXYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (BEDICED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS YDDOLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE. SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-LINKED CHAINS.

TISSUE SPECIFICITY: Plasma.

MISCELLANEOUS: CONTRARY TO THE RAT PROTEIN, WHICH IS AN ACUTE PHASE PROTEIN, THIS PROTEIN IS ALWAYS PRESENT AT HIGH LEVELS IN CITCHTATION
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SIMILARITY: TO OTHER PROTEINS OF INCLUDING COMPLEMENT COMPONENTS
                                                                          ; PF00207; A2M; 1.
; PF01835; A2M N;
ITE; PS00477; ALPH
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                                              Polymorphism;
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                                            ALPHA 2 MACROGLOBULIN; 1.
nhibitor; Glycoprotein; Plasma;
ymorphism; Thioester bond.
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ALPHA-2-MACROGLOBULIN
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                                       LPELPGEYSMKVTGEGCVYLQTSLKYNI------LPEKEEFPFALGVQTLPQTCD
                                                                           ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQFAFDLDVAVK---ENKD
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           use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89160243; PubMed-2466233;
Kunz D., Zimmermann R., Heisig M., Heinrich P.C.;
"Identification of the promoter sequences involved in the interleukin-6 dependent expression of the rat alpha 2-macroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-164 FROM N.A. STRAIN=Wistar; TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of its messenger RNA.";
J. Biol. Chem. 262:446-
[2]
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Kan C.-C., Chain A.C., Noonan D.J., Fey G.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-2-macroglobulin precursor (Alpha-2-M).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of DNA complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (an C.-C., Chain A.C., Noonan D.J., Fey G.H.,
Sequence of rat liver alpha 2-macroglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                    BIOÌ. Chem. 260:14224-14229(1985).

FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BALT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCADED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPED ENZYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-
                                                                                                                                                                                 LINKED CHAINS.
TISSUE SPECIFICITY: Plasma.
INDUCTION: BY INFLAMMATORY STIMULUS THE LEVEL
                                                                            European Bioinformatics Institute.
                                                                                                                                        FIRST INCREASES, THEN DECREASES AFTER A MAXIMUM.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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                                                                                       SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo
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EMBL; X13983; CAA32164.1; -.
EMBL; X13984; CAA322164.1; JOINED.
EMBL; X13985; CAA332164.1; JOINED.
EMBL; M11792; AAAA0637.1; -.
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                                                                                                                                                                                                                               RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQW
                                                                                                                                                                                                                                                                                                           TASN--LTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEI--YELRVTGRTQDEILFSNST
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                                                     ITILEEEMNVSVCGIYTYGKPVPGRVTVNICRKYSNPSNCFGEESVAFCEKLSQQLDGRG
                                                                                       CSMNSKHLNGTITAKYTYGKPVKGDVTLTFL----PLSFWGKKKNI---
                                                                                                                           QNFNLEGGLKQLSFPLSSEPTQGSYKVVIRTESGRTVEHPFSVEEFVLPKFEVRVTVPET
                                                                                                                                                               LSQQSDLGVISKTFQLSSHPILGDWSIQVQV-NDQTYYQSFQVSEYVLPKFEVTLQTPLY
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 DYTVKVTGEGCVYLQTSLKYSV---
                                                                                                                     LWYQPQATSAEVEMTAYVLLAYL----TTEPAPTQEDLTAAMLIVKWLTKQQNSHGGFSS
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                            AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK----ENKDDLNHV
                                                                                                                                                                                RGGAGGSHVYTKALLAYAFALAGNQDTKKEILKSLDEEAVKEEDSVHWTRPQ-KPSVSVG
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                                                         TQDTVVALHALSKYGSATFTRAKKAAQVTIRSSGTFSTKFQVNNNNQLLLQRVTLPTVPG
                                                                                       TODTTVALKALSER+ AALMNTERTNI QVTVTGPSSPSPLAVVQ-----
                                                                                                                                                  --WOPR--SLDIEVAAYALLSHFLQFQTSEGIP------
                                                                                                                                                                                                            -- SRGISDNYTLALITYALSSVGSPKA-KEALNMLTWRAEQEGGMQFWVSSESKLSDS--
                                                                                                                                                                                                                                          DNGCFRSSGSLLNNAMKGGVEDEVTLSAYITIALLEMSLPVTHPVVRNALFCLDTAWKSA
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Pfam; PF01835; A2M N; 1.
PROSITE; P800477; ALPHA 2 MACROGLOBULIN;
Serine protease inhibitor; Glycoprotein;
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Thioester

bond

1. Plasma;

Bait region; Signal;

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1476 734 86 276 288 555 773 680

MURINOGLOBULIN 1
BAIT REGION (APP
BY SIMILARITY.

(APPROXIMATELY)

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OVERDETS L., TOTTERENDS S., VAN LEUVEN F., VAN den Berghe H.;

OVERDETS L., TOTTERENDS S., VAN LEUVEN F., VAN den Berghe H.;

OVERDETS L., TOTTERENDS S., VAN LEUVEN F., VAN den Berghe H.;

"Molecular characterization of the murinoglobulins.";

J. Biol. Chem. 266:16903-16910(1991).

1. Biol. Chem. 266:16903-16910(1991).

1. FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTECULASIS IN THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTER SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE TETREAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUPFICIENTLY STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.
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P28665;
01-DEC-1992
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01-NOV-1995 (Rel. 32, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Murinoglobulin 1 precursor (MuG1).
MUG1 OR MUG-1.
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
HSSP; P01023; 18V8.
MGD; MGI:99837; Mugl.
InterPro; IPR002890; A2M N.
InterPro; IPR001599; MacTogloblnA2.
                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER:
TISSUE SPECIFICITY: Plasma.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACRO SIMILARITY: TO OTHER COMPONENTS C3, C4, AND C5.
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                                                                                                                              M65736; AAA73048.1;
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Rodentia;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                             LCVCTAALA-----VAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKT
                                                                          LVMAQGSIIQTGNHTHQVEPGEAPVKGKFALEIPVEFSMVPMAKMLIYTILPDGEVIADS
                                                                                                                                                      RHASAKHVAYAVYSLSKSYIYLDTETSSILPCNQIHTVQAHF--ILKGDLGVLKELIFYY
                                                                                                                                                                                                            WSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKA------YFLGS
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   LVPHGTEKDVYRYVEDMGLTAFTNLMIKLPIICFDYGMVPISAPRVEFDLAFTPEISWSL
                                                                                                                                   MVVSRGQLVAVGKQNSTM-------FSLTPENSWTPKACVIVYYIEDDGEIISDV
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Pred. No. 3.8e-69;
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RESULT 5
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ID A2M2 MOUSE
ID 24, Created)
DT 01-DEC-1992 (Rel. 24, Last seque)
DT 01-DEC-1992 (Rel. 24, Last seque)
DT 15-SEP-2003 (Rel. 42, Last annot.
DE Murinoglobulin 2 precursor (MuG2 MUG2 OR MUG-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cr.
OC Mammalia; Eutheria; Rodentia; Sc NCBI TaxID=10090;
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                                                                 sequence update)
annotation update)
(MuG2).
                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
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"Molecular characterization of the murinoglobuling.";
J. Biol. Chem. 266:16903-16910(1991).

1- Biol. Chem. 266:16903-16910(1991).

1- FUNCTION: A PROTEZINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTER SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE TETRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIENTLY STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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HSSP; P01023; 1BV8.
MGD; MGI:99836; Mug2.
InterPro; IPR002890; A2M_N.
InterPro; IPR001599; MacrogloblnA2.
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MEDLINE=91358495; PubMed=1840592;
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TISSUE SPECIFICITY: Plasma.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN
INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
                                                                            13
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                                                                                                                                      Similarity
                                                                            LCVCTAALAVAPG-----PRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKT
  ASNLTVSVLEAEG---
                                        LCLFSVLLAFLPSASSLNGDSKYMVLVPS-----QLYTETPEKICLHLYHLNE
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                                                                              FAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFG--NYDPSGST
                                                                                                                                    SDAEIS---EKWSLVLPPTVVKDSARAHFSVMGDILSSAIKNTQNLLHMPYGCGEQNMVL
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                                                          FAPNIYYLKYLDKTQQLTQKIKTKALGFLRAGYQRELNYKHKDGSYSAFGDQNGEREGNT
                                                                                                                                                                          TUNRLOSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGEQNMIN
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                                                                                                                                                                                                                                                                                            MNYLPTSMRMSVQLEASPDFTAVPVGDDHDSYCLSANGRHTSSWLV------TP
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RESULT 6
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SEQUENCE FROM N.A.
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MEDLINE=91113734; PubMed=1989698;
MEDLINE=91113734; PubMed=1989698;
Devriendt K., van den Berghe H., Cassiman J.-J.
"Primary structure of pregnancy zone protein.
"primary structure of pregnancy zone protein.
"In Biophys. Acta 1088:95-103(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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MEDLINE=86059456; PubMed=2415522;
Sand O., Folkersen J., Westergaard J.G., S
"Characterization of human pregnancy zone
                                                                                                                       Marynen P., Devriendt K., van den Berghe H., Cassiman J.-J.;
"A genetic polymorphism in a functional domain of human pregnancy
zone protein: the bait region. Genomic structure of the bait doma
of human pregnancy zone protein and alpha 2 macroglobulin.";
FEBS Lett. 262:349-352(1990).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 670-759.

MEDLINE=89380162; PubMed=2476433;

Sottrup-Jensen L.,

Sottrup-Jensen L.,

"The alpha-macroglobulin bait region. Seque
localization of cleavage sites for proteins
alpha-macroglobulins.";
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                             SEQUENCE OF 974-983.
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  Sottrup-Jensen L.;
e protein. Comparison with
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ein. Molecular cloning
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ence diversity and
ases in five mammalian
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Blochemistry 28:9324-9331(1989).

-i- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (BOLDED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

-i- SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. [5]
                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       Genew; HGNC:9750;
MIM; 176420: -
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Pfam; PF01835; A2M_N;
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EMBL; M24416; AAA60234.1; -.
EMBL; X51541; CAA35919.1; -.
PIR; S13495; S13495.
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Gene 81:325-334(1989).
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Cassiman J.-J., Marynen
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J. Biol. Chem. 260:15723-15735(1985).
              CARBOHYL
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InterPro; IPR002890; A2M_N.
InterPro; IPR001599; MacrogloblnA2.
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     ILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGE
                                                                                                                                                            RGEVFTLKATVLNYLPKCIRVSVQLKASPAF----LASQNTKGEESYCICGSE-RQTLS
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> Q (IN REF. 2).
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                                   TISSUE_Egg white;
TISSUE_Egg white;
MEDLINE_83238315; PubMed=6408074;
MEDLINE_83238315; PubMed=6408074;
Magase H., Harris E.D. Jr., Woessner J.F., Brew K.;
Magase H., a novel proteinase inhibitor from chicken egg white. I
"Ovostatin: a novel proteinase inhibitor from chicken egg white. I
Purification, physicochemical properties, and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P20740;
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                             J. Biol.
[3]
                                                                                                                                                                                                                                                                                                                 "Amino acid sequence of hen cloned cDNA.";
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     SEQUENCE OF 976-1028
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EMBL; X78801; CAA55385.1; ALT_INIT.
PIR; I50671; A20872.
HSSP; P01023; 1BV8.
GO; GO:0017114; F:wide-spectrum prote
InterPro; IPR002890; A2M_N.
InterPro; IPR001599; MacrogloblnA2.
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MEDLINE=93192299; PubMed=7680577;
Nielsen K.L., Sottrup-Jensen L.;
"Evidence from sequence analysis that hen egg-white ovomacroglobulin "Evidence from sequence analysis that hen egg-white ovomacroglobulin thiol is devoid of an internal beta-Cys-gamma-Glu thiol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: CONTAINS 56 MOL GLUCOSAMINE PER MOL SUBUNIT. SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY, INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                             EYDTINTTIFEKNTTTSNGLQCLNFMIPPVTSVSLAFISFTAKGTTFDLKERRSVMIWNM
                                                        EAB----GVFEKGSFKTLTLPSL-----PLNSADEIY-ELRVTGRTQD-----EILFSNS
                                                                                 AAAGKEPEPQYVLMVPAVLQ------SDSPSQVCLQFFNL----NQTISVRVVL
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|---IREFFPETWIWDIILINSTG---KASVSYTIPDTITEWKASAFCVEELAGFGM-SVP
EFSRGISDNYTLALITYALSSVGSPKAKEA-LNMLTWRAEQEGGMQFWVSSE-----:
                                        RQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWL
                                                                                                                                                            ATLTAFQPFFVDLTLPYSIIHGEDFLVRANVFNYLNHCIKINVLL--
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                                                                                           VSGYQKQLSYKHPDGSYSTFGIRDKEGNTWLTAFYYKSFAEASRFIYIDDNVQAQTLIWL
                                                                                                                                                SVVGDIMGTAIQNVHQLLQMPFGNGEQNMVLFAPNIYVLDYLDKTRQLSEDVKSKTIGYL
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                                                                                                                                                                                                                             SPTASDAVTOMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQI
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A2MG MOUSE
Q61838; Q60628;
Q1-NOV-1997 (Re
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Umans L., Serneels L., Hilliker C., Stas L., Overbergh L.,
de Strooper B., van Leuven F., van den Berghe H.;
"Molecular cloning of the mouse gene coding for alpha 2-macroglobulin
and targeting of the gene in embryonic stem cells.";
Genomics 22:519-529(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The primary sequence and the subunit structure of mouse alpha-2-macroglobulin, deduced from protein sequencing of the isolated subunits and from molecular cloning of the cDNA."; Eur. J. Biochem. 210:319-327(1992).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-NOV-1997 (Rel. 35,
15-SEP-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                     FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASES. THE ENTRAPPED ENZYME REMAINS ACTIVE AGALNST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS TUDROLYZED AND MEDIATES THE GREAT SUBSTRATES THE BAIT REGION AND MEDIATES THE
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                                                    IN CIRCULATION. SIMILARITY: TO OTHER
                                                                                                      COVALENT BINDING OF THE PROTEIN TO THE TISSUE SPECIFICITY: Plasma.

DEVELOPMENTAL STAGE: CONTRARY TO THE RA
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                                    SIMILARITY: TO OTHER PROTEINS OF INCLUDING COMPLEMENT COMPONENTS
                                                                                        ACUTE PHASE PROTEIN,
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                                                                                      RAT PROTEIN, ALWAYS PRESE
                                                      ALPHA-MACROGLOBULIN FAMILY,
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00207; A2M; 1. Pfam; PF01835; A2M N; 1 PROSITE; PS00477; ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:87854; A2m.
GO; GO:0016975; F:alpha-2 macroglobulin; NAS
InterPro; IPR002890; A2M N.
InterPro; IPR001599; MacTogloblnA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S27001; S27001.
HSSP; P01023; 18V8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M93264; AAA39508.1; -. EMBL; U06977; AAA87890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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 181
                    184
                                        121
                                                            125
                                                                                                                                                               418;
                                                                               67
                                                                                                  67
                                                                                                                                           24
                                                                                                                                                                         Similarity
LAGGLHQLSFPLSVEPALGIYKVVVQKDSGKKIEHSFEVKEYVLPKFEVIIKMQKTMAFL
                                                                                                 SNLTVSVLEAEGYFEKGSF--KTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSF
                 SDLGVISKTFQLSSHPILGDWSIQVQVND-QTYYQSFQVSEYVLPKFEVTLQTPLYCSMN
                                                                                                                      PTPAFLLLFLLLPRDATTATAKPQYVVLVPSEVYQESLKRPCVSLNHVNETVMLSLTLEY
                                                                                                                                          PGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQV------
                                                           ETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQWLSQQ 183
                                                                                AMQQTKLLTDQAV-DKDSFYCSPFTISGSPLPYT--FITVEIKGPTQ---RFIKKKSIQI
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1003
1385
1443
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568
                                                                                                                                                               Conservative
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91
144
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27.0%;
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BY SIMILARITY.
                                                                                                                                                                                                                                                         N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                          Pred.
                                                                                                                                                                                                                         QESLKRP -> SGIPEKA
I -> V (IN REF. 2).
VKF -> GII (IN REF.
                                                                                                                                                                                  Score 1373.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-2-MACROGLOBULIN 165 kDa SUBUNIT ALPHA-2-MACROGLOBULIN 35 kDa SUBUNIT.
                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                    Isoglutamyl cysteine
(By similarity).
                                                                                                                                                                                                                  ₽P ->
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                                         VKFRVVSVDISFRPLNETFPVVYIETPKRNRIFQWQNIH
                                                                                                                                                               Mismatches
                                                                                                                                                                                                       0D215688E80B4CCB
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Plasma;
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                                                                                                                                                                                                                                                                                                                                                              GYQRELLYQREDGSFSAFGNY---DPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTW
                                                                                                                                                                                                                                                                                                                                                                                                                                     LGDILGSAMQNLQNLLQMPYGCGEQNMVLFVPNIYVLNYLNETQQLTEAIKSKAINYLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHS--LFKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LKFTKVNTNYRPGLPFSGQVLLVDEKGKPIP----NKNITSVVSPLGYLSIFTTD
                                                                                                                                                                                        SEFSRGISDN----YTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFWVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHKDTVVKSVIVEPEGIEKEQTYNTLLCPQDTELQD---NSSLELPPNVVEGSARATHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SST-ISLQAFQPEFLELTLPYSVVRGEAFTLKATVLNYMSHCIQIRVDLEISPDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTPVELQAFQPFF1FLNLPYSVIRGEEFALEIT1FNYLKDATEVKVI1EKSDKFD1LMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TVRXYFPETWIWDLVPLDVSGD----GELAVKVPDTITEWKASAFCLSGTTGLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQEFQHYPAMGGVAPQALAVAASGPGSSFRAMGVPMMGLDYSDEI----NQVVEVRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPSAQSLPASDTHLKVKAA-PLSLCALTAVDQSVLLLKPEAKLSPQSIYNLLPGKTVQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKTYIQLKT-----RDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHGLANI-SIDTSNFTAP----FLRVVVTYKQNHVCYDNWWLDEFHTQADHSATLVFSP
SLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPS--
                                             QKVKALSFYQPRAPSAEVEMTAYVLLAYLTSESSRPTRDLSSSDLSTASKIVKWISKQQN
                                                                                          SESKLSDSWOPR--SLDIEVAAYALLSHFLQFQT-----
                                                                                                                                          TAWA-SISQSQESHVYTKALLAYAFALAGNKAKRSELLESLNKDAVKEEDSLHWQRPGDV
                                                                                                                                                                                                                                          LSMKQKENGCFQQSGYLLNNAMKGGVDDEVTLSAYITIALLEMPLPVTHSAVRNALFCLE
                                                                                                                                                                                                                                                                                     LKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLE
                                                                                                                                                                                                                                                                                                                                        GYQRQLNYQHSDGSYSTFGNHGGGNTPGNTWLTAFVLKAFAQAQSHIFIEKTHITNAFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTA---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGSSPHVRKHFPETWIW----LDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LAVPVGGHENSHCICGNERKTVSWAVTPKSLGEVNFTRTAEALESQELCGNKLTEVPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTK---
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SPSPLAVVO
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            InterPro; IPRO01134; Netrin_C.

Pfam; PF01207; AZM, 1.

Pfam; PF01835; AZM, 1.

Pfam; PF01831; ANATO; 1.

Pfam; PF01831; ANATO; 1.

Pfam; PF01759; NTR; 1.

PF0D0m; PD003264; Anaphylatoxin; 1.

SMART; SM00104; ANATO; 1.

SMART; SM00104; ANATO; 1.

SMART; SM00643; C345C; 1.

SMART; SM00643; C345C; 1.

PROSITE; PS0177; ALPHA 2 MACROGLOBULIN; 1.

PROSITE; PS0177; ANAPHYLATOXIN 1; 1.

PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMJA

CO3 LAMJA

STANDARD;

PRT; 1673 AA.

Q00685;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Complement C3 precursor [Contains: C3A anaphylatoxin]

C3.
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete complementary DNA sequence of complement of lamprey. Implication for to containing proteins.";
J. Immunol. 148:3290-3295(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petromyzontiformes;
NCBI_TaxID=94989;
                                                                                                                                                                                                                                                           PIR; I50806; I50806.
HSSP; P01024; 1C3D.
                                                                                                                                                                                                                                                                                               EMBL; D10087; BAA00983.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lampetra japonica (Japanese lamprey) (Entosphenus japonicus)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoar
                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOTH PROTEINS.
SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
SIMILARITY: Contains 1 anaphylatoxin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. AFTER ACTIVATION (C3B), IT CAN BIND COVALE VIA ITS REACTIVE THIOLESTER, TO CELL SUFFACE CARBOHYDRATES OF IMMUNE AGGREGATES. CYCLOSTOWATES C3 APPEARS TO REPRESENT THE COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES
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                                                                                                                                                                                       IPR000020; Anaphylatoxin.
IPR001599; MacrogloblnA2.
IPR001134; Netrin_C.
                                                                                                                                                                                                                                         IPR002890; A2M
                                                                                                                                                                                                                                                                                                                              equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petromyzontidae; Lethenteron.
Plasma; Inflammatory response; Glycoprotein;
                                                                                                                                                                                                                                                                                               .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
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                                                                                                         ---PSNEQGELVYTAQKYASASYMHIDV-TRIMRLGETLNVFLTAKTTQLNAVTHFTYMV
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                  PRQLSMLQIRREAEKYTQEFRKCCVDGLKMSPTGQGCEERLKRVTGPKECVDAFLQCCKK
                                                        VWKAMETFDTGCTAEGGAGRPGVFSDAGLALITSKGL-----NTTDRSEIGCPKVPSRK
                                                                                                                                                                                             AYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGN----KRLKELSYMV
                                                                                                                                                                                                               KEVDVVAKVQVGSAT----INPQKMRTDSNGLTSFTVTPPNVNQLTVTVRTDERH----
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COMPLEMENT C3.

COMPLEMENT C3.

BETA CHAIN (BY SIMILARITY).

ALPHA CHAIN (BY SIMILARITY).

GAMMA CHAIN (BY SIMILARITY).

C3A ANAPHYLATOXIN (BY SIMILARITY).

BY SIMILARITY.

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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By
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(By similarity).
W; 4B5FC756B123A506 CRC64; .
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---HFPETWIW--LDTNMGYRIYQEFE
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MALMEVNILSGFMVP--SEAISLSETVKK----VEYDHGKLNLYLDSVNETQ-FCVNIPA
KQMLRSDMIQPVTASVYDYYSPADKCTRLYNLPGGYVELSPLCQNDLCQCVEVSCPAK
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                                                                                                                      MTIIEVNMLTGF-IPDKNDLIQLKESVDKYISNYEITDSVLIIYWDKVPSTEDYCFAFKI
                                                                                                                                                                                                                                            KVTMTEADDGESPQGRLGWFDGKRRRRRDIGDEGGVEAVYRMMCTRYKPRKEDLSSESG
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                                                            VRNFKVSNTQDASVSIVDYYEPRRQAVRSYN---SEVKLSS-C--DLCSDVQGCRPCE 1400
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RESULT 10
CO4 HUMAN
STANDARD; PRT; 1744 AA.
ID CO4 HUMAN
AC PO1078; Q13160; Q13906; Q14835; Q9NPKS; Q9UIP5;
DT 21-UUL-1986 (Rel. 01, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT Complement C4 precursor [Contains: C4A anaphylatoxin].
Complement C4 precursor [Contains: C4A anaphylatoxin].
GN C4A AND C4B.
OS Homo sapiens (Human).
OC Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (C4A AND C4B).
RC TISSUE-Liver;
RX MEDLINE=84156544; PubMed=6546707;

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SEQUENCE OF 1-21 FROM N.A.

MEDLINE-9428204; PubMed-8012361;
Sargent C.A., Anderson M.J., Hsieh
Gomez-Escobar N., Campbell R.D.;

"Characterisation of the novel gene
complement C4A gene in the human ma
hum, Mol. Genet. 3:481-488(1994).
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21-hydroxylase gene.";
7 Tmmunol. 146:1057-1066(1991).
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Banta A.,
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Harrison R.A., Thomas M.L., Tack B.F.;
"Sequence determination of the thiolester site of
component of human complement.";
Proc. Natl. Acad. Sci. U.S.A. 78:7388-7392(1981).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=85156269; PubMed=3838531; Belt K.T., Yu C.Y., Carroll M.C., "Polymorphism of human complement
                                                                                                                                                                                                                                                             MEDLINE=82182029; PubMed=6978711; Campbell R.D., Gagnon J., Porter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete sequence of the complement C4AQO, C4B1, DR3 haplotype."; Immunogenetics 43:250-252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=91108039;
                  Hortin G., Sims H., Strauss A.W.;
"Identification of the site of sulfation
                                       MEDLINE=86111851;
                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                            human
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[7]
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em. J. 199:359-370(1981).
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, Swartzell S., S
e determination of
                                                                                                                                                                                                                                                                                                        31264286; PubMed=6167582; , Gorski J.P., Hugli T.E.; e primary structure of human Chem. 256:8685-8692(1981).
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tural basis of
                                       1405-1431, AND SULFATION 11851; PubMed=3944109;
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PubMed=1988494;
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nd D.C., Christi
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Genew; HGNC:1323; C4A. Genew; HGNC:1324; C4B. HSSP; P01031; 1KJS. SWISS-2DPAGE; P01028;

HUMAN.

GO: 0005576; GO: 0006958;

C:extracellular; NAS. P:complement activati

activation,

classical pathway;

120790;

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EMBL; KO2403; AAB59537.1; -.
EMBL; KO2404; AAA55651.1; -.
EMBL; KO2404; AAA51855.1; -.
EMBL; M59815; AAA51855.1; JOINED.
EMBL; U24578; AAA59717.1; -.
EMBL; AC019413; AAB67980.1; -.
EMBL; AL049547; CAB89302.1; -.
EMBL; AL049547; CAB89302.1; -.
EMBL; M14823; AAA5292.1; -.
EMBL; M14824; AAA52677.1; -.
EMBL; X77491; CAA54627.1; -.
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-I- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4, C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES.

-I- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER OF MONIDERICAL CHAINS (ALPHA, BETA, AND GAMMA).

-I- POLYMORPHISM: HUMAN COMPLEMENT COMPONENT C4 IS POLYMORPHIC WITH AT LEAST TWO LOCI, C4A AND C4B. 13 ALLELES OF C4A AND 22 ALLELES OF C4B HAVE BEEN DETECTED. THE ALLELES CARRY THE BLOOD GROUP RODGERS WHILE THE C4B ALLELES CARRY THE BLOOD GROUP RODGERS WHILE THE C4B ALLELES CARRY THE BLOOD GROUP CHIDO.
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Yu C.Y., Belt K.T., Giles C.M., Campbell R.D., Porter in Structural basis of the polymorphism of human compleme C4A and C4B: gene size, reactivity and antigenicity."; EMBO.J. 5:2873-2881(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the defect.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
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Anderson M.J., Mi
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STRUCTURAL BASIS OF POLYMORPHISM
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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SIMILARITY:
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MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: C4 PLAYS A CENTRAL ROLE IN CLASSICAL PATHWAY OF THE COMPLEMENT SACTIVATED C1 WHICH REMOVE FROM THE AL
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DE ANTIGENS WHILE C4B ALLOTYPES
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SMART; SM00104; ANATO; 1.
SMART; SM00643; C345C; 1.
PROSITE; PS00477; ALPHA 2 MACROGLOBULIN;
PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
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GO; GO:0006937; P:regulation of muscle contraction; NAS.
InterPro; IPR0002890; AAM N.
InterPro; IPR00020; Anaphylatoxin.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
Pfam; PF00207; AAM; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01821; ANATO; 1.
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Inflammatory response; Polymorphism; Disease
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                                                                   LYCSMNSKHLNG---TITAKYTYGKPVKGDVTLTFLPLSFWGKKKNI----TKTFKINGS
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 GNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPS--K
                      PFSLDLSKTKRHLVPGAPFLLQALVREMSGSP-----ASGIPVKV-----
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Pred. No. 2.8e-46;
0; Mismatches 636
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                                  TYNVLDMKNTTCQDLQIEVTVKGHVEYTMEANEDYEDYEYDELPAKDDPDAPLQPVTPLQ
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RESULT 11
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN.EM; TISSUB=Liver;

MEDLINE=85289294; PubMed=2993295;

Nonaka M., Nakayama K., Yeul Y.D., Takahashi M.;

"Complete nucleotide and derived amino acid sequences of the component of mouse complement (C4). Evolutionary aspects.

J. Biol. Chem. 260:10936-10943(1985).
                                                                                    SEQUENCE OF 1099-1142 FROM N.A. STRAIN=B10.WR, C57BL/6, C3H/He, CMEDLINE=90353398; PubMed=2387317;
                                                                                                                                     "Isolation of cDNA clones specifying complement and its isotype, sex-limit Proc. Natl. Acad. Sci. U.S.A. 81:6822
                                                                                                                                                                                                                                                                                                                                               "Sequence
J. Biol. C
                                                                                                                                                                                                                                                                                                                                                              Ogata R.T., Rosa P.A., Zepf N.E.; "Sequence of the gene for murine complement component C4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87309760; PubMed=3624865; Rosa P.A., Sepich D.S., Robins D.M., (Constitutive expression of Slp genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=85298264; PubMed=3862104;
Sepich D.S., Noonan D.J., Ogata R.T.;
"Complete cDNA sequence of the fourth
SEQUENCE OF
                                                                                                                                                                                                                  SEQUENCE OF 651-810 AND 924-1083 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=B12.WR; TISSUE=Liver; MEDLINE=89380278; PubMed=2777798;
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                                                                                                                                                                                                       MEDLINE=85038607; PubMed=6208559;
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Immunol. 139:1568-1577(1987).
                                               region
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                      Immunol.
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1105-1449
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sh and C4-low m
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                      20:1607-1610(1990).
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                                               mouse
the is
                                                                                                                                      pecifying the fourth component of mouse
    sex-limited protein.";
A. 81:6822-6826(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82:5895-5899(1985).
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                                                isotype-specific
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                                                            strains have identical
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EMBL; PIR; A PIR; A

A24558; A29176;

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EMBL; K00019; AAA39554.1; EMBL; M11729; AAA39550.1; EMBL; M12968; AAA39555.1; EMBL; M12970; AAA39555.1; EMBL; M12972; AAA39555.1; EMBL; M12972; AAA39557.1; EMBL; M1789; AAA39557.1; EMBL; K02798; AAC42021.1; EMBL; K02798; AAC42021.1; EMBL; M14226; AAA39561.1; EMBL; M14226; AAA39564.1; EMBL; M14226; AAA39564.1; EMBL; M14226; AAA39684.1; EMBL; X55493; CAA39112.1; EMBL; X55493; CAA39112.1; EMBL; X55493; CAA39114.1;
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MEDLINE=83273751; PubMed=6192448;

MEDLINE=832751; PubMed=6192448;

MEDLINE=83275151; PubMed=619248;

MEDLINE=83275151; PubMed=6192448;

MEDLINE=83275151; PubMed=619248;

MEDLINE=83275151; PubMed=619248;

MEDLINE=8327515151; PubMed=619248;

MEDLINE=8327515151; PubMed=619248;

MEDLINE=8327515151; PubMed=619248;

MEDLINE=83275151; PubMed=619248;

MEDLINE=8327515151; PubMed=619248;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 83:7883-7887(1965).
-i- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF CLASSICAL PATHAX OF THE COMPLEMENT SYSTEM. IT IS PROCE ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Slp genes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tosi M., Levi-Strauss M., Duponchel C., Meo T.;
"Sequence heterogeneity of murine complementary DNA clones related
the C4 and C4-Slp isoforms of the fourth complement component.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:389-394(1984).
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAV
OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA)
MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANAPHYLATOXIN.
SUBUNIT: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Contains 1 anaphylatoxin-like domain.
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                                                                   Yokoyama S.,
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Pfam; PF001821; ANATO; 1.
Pfam; PF01759; NTR; 1.
Pfam; PF01759; NTR; 1.
ProDcm; PD003264; Anaphylatoxin; 1
SWART; SM00104; ANATO; 1.
SMART; SM00643; C345C; 1.
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InterPro; IPR000200; Anaphylatoxin.
InterPro; IPR001599; MacroglobinA2
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                                          PKS-NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVND---QTYYQSFQVSEYVL
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  PKFEVTLQTP-----LYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNI-
                                                                 ATE---TQGVNLLFSSRRGHIFVQTDQPIYNPGQRVRYRVFALDQKMRPSTDFLTITVEN
                                                                                                             GSCSPKKDFKLSSGDDFVLLSLEVPLEDVRSCGLFDLRRAPHIQLVAQSP---WLRNTAFK
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F -> Y (IN REF. 4).
G -> E (IN REF. 4).
Q -> E (IN REF. 5).
Q -> E (IN REF. 5).
DL -> AI (IN REF. 5).
P -> R (IN REF. 5).
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D -> E (IN REF. 7).
A -> T (IN REF. 7).
A -> Y (IN REF. 4).
G -> S (IN REF. 4).
G -> S (IN REF. 4).
G -> Y (IN REF. 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
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Pred. No. 4.8e-46;
45; Mismatches 643; Indels 366;
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ANAPHYLATOXIN-LIKE.
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                                  --KASEDLRNVAHNSLMAMAEETGEHLYWGLVLGSQDKVVLRPTAPRSPTEPVPQAPALW
                                                       SPKAKEAL-----NMLTWRAEQEGGMQFW---VSSESK-LSDSWQPRS------LD
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RESULT 12
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between
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement C3-1 [Contains: C3A anaphylatoxin] (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Third component of trout complement. cDNA cloning of functional sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94065166; PubMed=8245455; Lambris J.D., Lao Z., Pang J., Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P98093;
01-FEB-1996
         InterPro; IPR002890; A2M N.
InterPro; IPR001020; Anaphylatoxin.
InterPro; IPR001159; MacrogloblnA2.
InterPro; IPR001114; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8022;
                                                                          HSSP; P01024; 1C3D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. 151:6123-6134(1993)
                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                             FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
                                                                                                                                                                                                                                                                     SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONCMY
                                                                                                                                                                                                                                                                                  SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                    RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1356
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                                                                                         ; L24433; AAB05029.1; ALT_INIT.
I51339; I51339.
PF00207;
                                                                                                                                          an
                                                                                                                                     and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVOPSSAVLYDYYSPDHKCSVFYAAPTKSQLLATLCSGDVCQCAEGKCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPLQLFEGRRSRRRE-----APKVAEEQESRVQYTVCIWRNGKLGLSGMAIAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IETTAYALLHLLLR----EGKGKMADKAASWLTHQGSFHGAFRSTQDTVVTLDALSAYWI
                                                                                                                                                                                                                                                                                                                 C3A ANAPHYLATOXIN & GENERATING C3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                 Contains 1 anaphylatoxin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGP-GRSGMALME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conservation
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Complement pathway; Complement alternate pathway; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD003264; Anaphylatoxin; SMART; SM00104; ANATO; 1. SMART; SM00643; C345C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01835; A2M N;
Pfam; PF01821; ANATO;
Pfam; PF01759; NTR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CROSSLNK
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             KDGKGVACLKKEHITQTFPKIHDLVKQSI----
                                                                                                      TLQTP---LYCSMNSKHLNGTITAKYTYGKPVKGDVTLTF
                                                                                                                                     TIFREI-VNPDKGVKSGQFKLPDIVSFGTWHVVTRFQSTPQKTFSSEFEVKEYVLPSFEV
                                                                                                                                                                                                  I--FIQTOKTIYTPASTVHYRVFSMTPGLEPLTREIFEDQEVAKNKEIAVSVEIMTPENI
                                                                                                                                                                                                                                  ISVFIQTDKALYKPKQEVKFRIVTLFSDFKPY-----
                                                                                                                                                                                                                                                                                                                              AALQV-----LSAPNLLRVGSNENIFVESQDHVGGPLNVKI-MVKNHPTQSKELASKS
                                                                                                                                                                                                                                                                                                                                                              AALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVLEAE
                                       -----KKKNITKTF-KINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT
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ilarity 24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
OF SIMILARITY.
N-LINKED (GLCNAC...).
[BOGlucamyl Cysteine thioester (Cys-Gln)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C3B (ALPHA' CHAIN).
C3C FRAGMENT (BY SIMILARITY).
C3G FRAGMENT (BY SIMILARITY).
C3G FRAGMENT (BY SIMILARITY).
C3D FRAGMENT (BY SIMILARITY).
C3F FRAGMENT (BY SIMILARITY).
C1F FRAGMENT (BY SIMILARITY).
CLEAVAGE (BY C3 CONVERTASE).
CLEAVAGE (BY FACTOR I) (BY SIMIL CLEAVAGE (BY FACTOR I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                           Score 984.5; DB 1;
Pred. No. 6.1e-46;
8; Mismatches 571;
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BETA CHAIN.
ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPERDIN-BINDING. INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE (BY FACTOR ANAPHYLATOXIN-LIKE.
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(BY SIMILARITY)
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                                                                                                             TVTGPSSPSPLAVVQPMAVNISANGFGFAICQLNVV---YNVKASGSSRRRRSI-----
                                                                                                                                                                                                                                                                                                                                                    YALSSVGSPKAKEALNMLTWRAEQ----EGGMQFWVSSESKLSDSWQPRSLDIEVAAYALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLGLHSIEVKASVKNSGSNDGVKRDLRVVAEGVLVKKETNVLLNPVKHGGEQT-SHIPSG
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                                                         EVAGRAS-----VTKWSIN-NKNQFHTRTDKVNSIDKDLTVKASGNGEATLSVVTLYYA
                                                                                                                                                                                                                                                                                                                                                                                                              MTAFVLIAMQEASSVCEQSVNSLPG-----SMAKAVAYLEKRLPH-LTNPYAVAMTS
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----QNQEAFDLDVAVKENKDDLNHVD----
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rPro; IPkvvii. (; PF00207; A2M, 1. n; PF01835; A2M_N; 1.

Netrin_C. Anaphylatoxn. MacrogloblnA2 Anaphylatoxin. A2M N.

ProDom; PD003264; Anaphylatoxin; 1.

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Elapidae; Elapinae; Naja.
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                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3A anaphylatoxin and generating C3B (beta chain + alpha' chain) (By similarity).

SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
SIMILARITY: Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM, ITS PROCESSING BY C3 CONVERTAGE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAWMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR DERMEABILLTY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
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(Rel. 26, Last sequence update)
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SMART; SM00643; C345C; 1.
SMART; SM00643; C345C; 1.
PROSITE; PS00477; ALPHA 2 MACROGLOBULIN;
PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
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    VSRGQLVAVGK-----
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                                                                   RQAIKSMTATAYQTQGGSENYLHVAITSTEİKPĞDNLEVNENVRĞNANSLNQIKYFTYLI
                                                                                                                                                                                                         VITVTQRNYTEYWSGSNSGNQKMEAVQKINYTVP---QSGTFKIEFPILEDSSELQLKAY
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DESCRIPTION OF THE PROPERTY OF
                  PIR; S15764; C3RT.

PDB; 1QQF; 31-JUL-00.

PDB; 1QSJ; 31-JUL-00.

InterPro; IPR002890; A2M N.

InterPro; IPR002020; Anaphylatoxin.

InterPro; IPR001599; MacrogloblnA2.

InterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "ESTITOGEN REGULATION OF tissue-specific expression of complement C3.";
J. Biol. Chem. 264:16941-16947 (1989).

-IF FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
-IF FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUROCYTES.
-ISUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA')
                                                                                                                                                                                                                                                                                                                                                                   use
                                                                                                                                                                                                         EMBL; X52477; CAA36716.1;
EMBL; M29866; AAA40837.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification, characterization, and anaphylatoxin (C3a).";
Biochemistry 17:5031-5038(1978).
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STRAIN-Wistar; TISSUE=Liver;
MEDLINE=90245672; PubMed=2336397;
Misumi Y., Sohda M., Ikehara Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement C3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1316-1595 FROM N.A. MEDLINE=89380332; PubMed=2674144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=79062262; PubMed=309768;
Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt R.A.,
Daniels J.S., Daughaday W.H., Bradshaw R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 671-748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide and
Nucleic Acids Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Estrogen
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                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN. SIMILARITY: Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                     veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                           non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.A., Komm B.S., Ponce-De-Leon H., Yi
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(Rel. 15, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Contains: C3A anaphylatoxin)
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institutions as long as its content
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CHAIN 25
CHAIN 671
PEPTIDE 671
PARIN 693 7,
SULFID 558 81
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TLFID 693 720
TLFID 1011 1158
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FID 1101 1158
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SMART; SM00104; ANATO; 1.
SMART; SM00643; C345C; 1.
PROSITE; PS00477; ALPHA 2 MACROG
PROSITE; PS01177; ANAPHYLATOXIN_
PROSITE; PS01178; ANAPHYLATOXIN_
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PF01821; ANATO;
PF01759; NTR; 1.
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BY SIMILARITY.

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BETA CHAIN.
ALPHA CHAIN.
C3A ANAPHYLATOXIN.
C3B (ALPHA' CHAIN).
CLEAVAGE (BY C3 CONVERTASE).
ANAPHYLATOXIN-LIKE.
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                        RPYTVAIAGYALALMNKLEEPYLTKFLNTAKDRNRWEEPGQQLY--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSELQGG----NKSPVTLTAYIVTSLLGYR---KYQPNI---DVQESIHFLESEFSRGIS
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                                          LMEVNLLSGFMVPSEAISLSET-----VKKVEYDHGKLN-----LYLDSVNET-QFCVNI
                                                                                                                                          NVKASGSSRRRRSIQNQEAFDLDVAV-----
                                                                                                                                                                                          HKDLNMDVSLHLPSRSSPTVFRLLWESGSLLRSEETKQNEGFSLTAKGKGQGTLSVVTVY
                                                                                                                                                                                                                                                                                     NVEATSYALLALLLKDFDSVPPVVRWLNDERYYGGGYGSTQATFMVFQALAQYRADVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HQEMIGGFRNTKEADVSLTAFVLIALQEARDICEGQVNSLPGSINKAGEYLEASY-LNLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYSVVRNEQVEIRAVLFNY-REQEKLKVRVELLHNPAFCSMATAKK----RYYQTIEIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYSVIRGEEFALEITIFNYLKDATEVKVIIE--KSDKFDILMTSSEINATGHQQTLLVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LTDNRLQS---TLKTLSFSFPPNTVTGSER---VQITAIGDVLGPSING--LASLIRMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LWVLTDANLTKDYIDGV-----
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21-JUL-1986
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                                                                                                                                                               SEQUENCE OF 25-41 AND 749-760.

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                                                                                                                                        Cancer Res.
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 658-761 FROM N.A. MEDLINE=84201365; PubMed=6609661;
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                                                                                                         ALTERNATIVE INITIATION. MEDLINE=95053742; PubMed=7964485;
                                                                                                                                                                                                                                                                         component of mouse complement.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       sequences of cloned cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85054819;
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Mammalia; 1
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"Amino acid sequences of
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Cancer Res. 53:4418-4423(1993)
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(Rel. 33, Last sequence update)
(Rel. 42, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                            421:307-312(1983)
                                                                                                                                                                                                                                                                                                                                                                                                  Domdey H.;
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Sciurognathi; Muridae;
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EMBL; K02782; AAC42013.1; -.
EMBL; J00369; AAA37336.1; JOINED.
EMBL; M33032; AAA37378.1; -.
EMBL; Z37998; CAA6099.2; -.
EMBL; A92459; C3MS.
HSSP; P01024; 1C3D.
MGD; MGI:88227; C3.
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Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
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                                                                                                                                                                                                                                                                                                                                     ProDom; PD003264;
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InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                 Inflammatory response;
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- MISCELLANEOUS: IC3B IS T TO FORM C3C AND C3DG. OT AS C3D OR C3G.
- SIMILARITY: TO C4, C5 AN SIMILARITY: Contains 1 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
Event=Alternative initiation;
Comment=2 isoforms, Long (shown
alternative initiation;
MISCELLANEOUS: C3B IS RAPIDLY SPLI
AND A COPACTOR TO FORM IC3B (INACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTECLYTIC DEGRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PREMERBILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES. THE SHORT ISOFORM HAS B-CELL STIMULATORY ACTIVITY.

SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha, chain, releasing C3A anaphylatoxin and generating C3B (beta chain, releasing C3A anaphylatoxin and generating C3B (beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in the statement is not removed. Usage by and for comtities requires a license agreement (See http://www.isb-sib.ch/an
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SM00643; C345C;
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1474	1414	1354	1301	1241	1196	1137	1077	1019	962	904	849	791	737	679
DASVSIVDYYEPRRQAVRSYNSEVKLSSCDLC 1390	PSEAISLSETVKKVEYDHGKLNLYLDSVNET-QFCVNIPAVRNFKVSNTQ 1358 ::: : : :	SIQNOEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNLLSGFMV 1309 : : : : : : : : :	PSSPSPLAVVQPMAVNISANGFGFAICQLNVVXNVKASGSSRRRR 1256	FLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAA-LMNTERTNIQVTVTG 1211	LSSYGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAAYALLSH 1152	NKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISDNYTLALITYA 1095 :: : ::: :	WISAFVLRCFLEADPYIDIDQNVLHRTYTWL-KGHQKSNGEFWDPGRVIHSELQGG 1041	APNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGST 986 : : : : : : :	STLKTLSFSFPDNTVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGEQNMINF 929	HLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQ 874 :	ITIFNYLKDATEVKVIIBKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLEPIRPT 825 :	BFEVTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALE 767 :	HDFSLGSSPHVRKHFPETWIWLDTNMGYRIYQ 707	GLWVLTDANLTKDYIDGVYDNAEYAERFMEENEGHIVDI 675

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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   DIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNT
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
GPI-anchored alpha-2 macroglobulin-related protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                      related protein.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AY083458; AAM00021.1; -.
InterPro; IPR002890; A2M N.
InterPro; IPR001599; MacrogloblnA2.
Pfam; PF00207; A2M; 1.
Pfam; PF00207; A2M; 1.
Pfam; PF00207; A2M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hashimoto M., Ichihara M., Takahashi M.; "Cloning and characterization of GPI-anchored related protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             MRSRRLLSAAHLLCLCAVALA-APGSRFLVTAPGIIRPGANVTIGVDLLENSPPQVLVKA
                                                                                                                                                                                                                                                                                                              MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
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                                                                                                                                                                                                                                                                                                                                                             Conservative 176;
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-DSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFF
                                                                                                                                                                                                                                                                                                                                                          72.9%; Score 5360; DB 11; 71.6%; Pred. No. 4.1e-318; tive 176; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                            161658 MW;
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EFSALVHKENTDIQLTVTGPGIPRSIHFRIDSQNLFLLHQEELHALDPITVNVSAHGSGF
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Matches 834;
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Q8NJA7;
01-OCT-2002 (TrEMBLrel. 22, Create
01-OCT-2002 (TrEMBLrel. 22, Last
01-MAR-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ALB34478; CAD39137.1; -. InterPro; IPR001599; MacrogloblnA2. Pfam; PF00207; A2M; 1. PR00SITE; PF00477; ALPHA 2 MACROGLOBULIN; 1. Hypothetical protein.

NON TER 1 1 1
SEQUENCE 854 AA; 95599 MW; 7B51863A2565C004 CRC64;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Melanoma;
Blum H., Bauersa
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                                                                                                                     RTYTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQES
                                                                                                                                                                                               KALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLH
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                                                                                                                                                                           KALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLH
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                                                                                                IQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQES
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Pred. No. 4.7e-254;
1; Mismatches 2;
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Catarrhini; Hominidae;
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Matches 657
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EMBL; AK095888; BAC04642.1; -. InterPro; IPR002890; AZM N.
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QBN915; QBN916; QBN9
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Homo sapiens (Human).
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Mammalia; Eutheria;
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Query Match
Best Local S
Matches 477
                                                                                        WormPep; ZK337.1a; CE16718.

WormPep; ZK337.1b; CE16719.

InterPro; IPR002890; AZM N.

InterPro; IPR000847; HTH_LysR.

InterPro; IPR001899; MacroglobinA2.

InterPro; IPR001917; NHtransf_2.

Pfam; PF00207; AZM; 1.

Pfam; PF01835; AZM N; 1.

PFROSITE; PS00599; AA TRANSFER CLASS 2; 1.

PROSITE; PS00599; AA TRANSFER CLASS 2; 1.

PROSITE; PS0044; HTH_LYSR PAMILY; 1.

PROSITE; PS00041; HTH_LYSR PAMILY; 1.

Alternative splicing; Hypothetical protein.

VARSPLIC 714 724 MISSING (IN IS

SEQUENCE 1519 AA; 168385 MW; 78139ACB56
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 168.4 kDa protein ZK337.1.
ZK337.1.
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Rhabditidae; Pelode;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases -- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ZK337.1B (SHOWN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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O46015; O46014;
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31.6%;
290;
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Caenorhabditis.
                         Pred.
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                                                                                                etical protein.
MISSING (IN ISOFORM ZK337.1A).
MW; 78139ACB564AB742 CRC64;
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  Mismatches
1850; DB 5;
No. 8.6e-104;
smatches 563;
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  Indels 180;
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Q8T398 PRELIMINARY; PRT; Q8T398; O1-JUN-2002 (TrEMBLrel. 21, Created O1-JUN-2002 (TrEMBLrel. 21, Last se O1-MAR-2003 (TrEMBLrel. 23, Last ar Alpha-2-macroglobulin homologue.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hepatopancreas;
Hammond J.A., Nakao M., Yano T., Kemp G.D., Smith V.J.;
"Complete cDNA of an alpha2 macroglobulin homologue with
histidine residue from Ciona intestinalis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ431688; CAD24311.1;
InterPro; IPR001064; CTystallin.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR00164; TSP1.
InterPro; IPR001084; TSP1.
                                                                                                                                                                                                                                      Pfam; PF00207; A2M; 1.

Pfam; PF01835; A2M N; 1.

SMART; SM00209; TSP1; 1.

PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; 1.

PROSITE; PS00225; CRYSTALLN BETAGAMMA; 1.

PROSITE; PS050025; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                  24.2%; Score 1779.5; DB 5; llarity 30.0%; Pred. No. 2.3e-99; Conservative 293; Mismatches 586;
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NARIYLENHLT-SISDNKYALAIVTYALHVAGSSRANEALLALEALATVQGGFKFWHDNS
                                                                                                                                                                                                                                                      LLVYGDILGSTMNNLGSLLRTPSGCGEQNMLGFAPDVFVTLYLHSAGKLDAATRAKAFKH
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                                                                                                                                                                  FOTGYSNELNYKHRDGSFSAFGEGDASGSTWLTAFAAKCFMFARELRPTL-VSASVIDQA
                                                                                                                                                                                                            MRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFL---EADPYIDIDQNVLHRT
                                                                                                                                                                                                                                                                          ITSSSTNIDAGEDVSIRVQTSSSGAYVGARAIDQSVLLLKSGNDVSQERIVTDLNKYSVT
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K., Evangelista C.C., Ferraez C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygol
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVGLLGVDQSVLLLKSGNDLSQDDIFNSLNIYQTS---TPWMNGYGRYPGQTSGLVTLTN
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                                                                                                                                                                                                                                                               KLESVARKENDRWWW----SKATESTGEDGRVFHWKPRSNDVEITSYVLLALLEKDPAEK
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                                                                                                                                                                                                                  SGPGRSGMALMEVNLLSGFMVPSEA---
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RX MEDLINE-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanarides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA Mank M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bazej R.G., Champe M., Pfeiffer B.D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davrage S., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davrage R., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davrage A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Ways A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Galan P., Harris M., Classer K.,
RA Rabria D., Houston K.A., Howland T.J., War I.M., Classer K.,
RA Rabria D., Houston K.A., Howland T.J., War I.M., Nix N., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Notland G.D., Warshar Y., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milahina N.V., Mobarry C., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milahina N.V., Mobarry C., Wang S., Yan M., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mary S. Mary S. Mary S., Sandar R., Shang G., Zhao Q., Zheng L.,
The
Ferriera S., Frise E
Gonzalez M., Houck J
Ibegwam C., Jalali M
McIntosh T.C., Moy P
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Q9VLZ0;
01-MAY-2000
01-OCT-2002
                                                                                                                                                                     SEQUENCE
Celniker
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                               Banzon J.,
                                                                                                                                              Evans C.A.,
                                                                                                           Carlson
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rr S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
a S., Frise E., Galle R.F., Garg N.S., George R.A.,
z M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
c., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
h T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
                                                                                                                                                                     S.E., Adams M.
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Last annotation update)
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Best Local :
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Pfam; PF01835; A2M; 1.
Pfam; PF01835; A2M; N; 1.
PROSITE; PS00477; ĀLPHĀ, 2_M;
PROSITE; PS00284; SERPIN; 1.
SEQUENCE 1397 AA; 155108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Mitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B. Phouanenavong S., Pittman G.S., Puri V., Richards S., Stapleton M., Strong R., Svirskas R., Tector C., Tyle Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., "Sequencing of Drosophila melanogaster genome.", submitted (MAR-2000) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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InterPro; IPR002890; !
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Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                           LNGTITAKYTYGKPVKGDVTLT------FLPLSFWGKKKNITKTFKINGSANFSFNDEE
                                                                                                                                                                                                                                                                GVISKTEQLSSHPILGDWSIQVQVN-DQTYYQSEQVSEYVLPKFEVTLQTPLYCSMNSKH
 NFEAPVNENGIATFNVRLPD-SDSRYYRIFASFDGSENTIGSISKFEPTPMSREPLKIQV
                              NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
                                                                                      VLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKI
                                                                                                                                                   MKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIJEFFDYTT
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                                                                                                                         --IIHWAQRG-
                                                                                                                                                                                     IKATIRAKYTYGKPVKGKATVSMERSYGYFGDLNANGNKQE--KTIDVDGKGHVEFD---
                                                                                                                                                                                                                                                 GVFSGELQLSEQPVLGTWKISVSVDGDNRETKSFEVDKYVLPKFEVIVDTPKAVVIADKV
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IPR000215; Serpin.
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e EMBL/GenBank/DDBJ
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.2e-94;
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RESULT 9
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                                                                                                                                                                               RRQAVRSYNSEVKLSSCDLCSDV---QGCR 1397
                                                                                                                                                                                                                                                                                                                 SFKVTPTVKDTPNQLLIVD--
                                                                                                                                                                                                                                                                                                                                                   AFDLDVAVKENKDDLNHVDLNVCTSF-----SGPGRSGMALMEVNLLSGFMVPSEA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIPANSGKSVSFMIRPKNVGFTTLKITÄTSALÄGDÄIHQKLKVEPEGVTLFENRAVFINL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAENVG---EBEFTLTKKIPDTITSWVVTGFSLNPTSGIALTKNPSKIRVFQPFFVSTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DT-NMGYRIYQEFEVT--VPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPKACVIVYYIEDDGBIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDS
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                                                                                                                                                                                                                                                                     ISLSETVKKVEYDH--GKLMLYLDSVNETQF-CVNIPAVRNFKVSNTQDASVSIVDYYEP
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                                                                                                                                                                                                                             IQAVDRVKRVETKNSDSTVVVYFDSLTPGDVRCLPLEASKAHAVAKQKPASVSLYDYYDT
                              PRELIMINARY;
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                              PRT;
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      RX MEDLINE 2019606; PabMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.P.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Mank K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Mari J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bandari D.J., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Brokstein P., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dun P.,
RA Gebrie C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Heiman T.J., Li Z., Liang Y., Lin X.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Kimmel B.E., Kolira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Heiman T.S., Pan M., Pacleb J.M.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Find B., Kalush F., Karpen G.H., Kez N., Morits J., Moshrefi A.,
Ra Hostin D., Hollishian N.V., Mobarry C., Morits J., Moshrefi A.,
Ra Hostin D., Hollishian N.V., Mobarry C., Morits J., Nelso
                                                                                                       Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Gayg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

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"Sequencing of Drosophila melanogaster genome.";

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
  Misra S., Crosby M.A.,
Hradecky P., Huang Y.,
Tupy J.L., Bergman C.,
                                                                     SEQUENCE FROM N.A.
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  Bayraktaroglu L., Car
Prochnik S.E., Smith
lson J.W., Celniker S.
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EMBL; AE003618; AAN1
SEQUENCE 1408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
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8 M.D., Celniker

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                                                                                                                                                                                                                                                                                                                                                                                                                                             HFEANKSFIYQVVVKNVDGSPVT--NSAKNVKIGF-DKSYSYFHEPSPK-----TRI
                                                                                                                                                                                                                                                                                                             --IIHWAQRG--QYLP----PIKLFAVVTEELTGNKQNATATVVLHQQRYSIEPYERPE
                                                                                                                                                                                                                                                                                                                              MKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTT
                                                                                                                                                                                                                                                                                                                                                        VLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKI
                                                                                                                                                                                                                                                                                                                                                                             LNGTITAKYTYGKPVKGDVTLT-----
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                     PETWIWLDTNMGYRI-YQEFEVT--VPDSITSWVATGFVISEDLGLGLTTTPVELQAFQP
                                                                                                                                  VPKATIYVYYVVNN-DLQFEEKTIDFEKEFSNSIDVS-APTNAKPSEEVKLRIK-TDADS
                                                                                                                                                       TPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDS
                                                                                                                                                                          NTKKPRLGEQVSFDVVSIEDLPYFVYTIVARGNVILSDYVDVPDGQKTYTV-KFTPTFSM
                                                                                                                                                                                                  RDENIKVGSPFELVVSGNKRLKELSYMVVSRGQL-----VAVGKQNSTMFSLTPENSW
                                                                                                                                                                                                                                            NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLVNATGIYSVVGPGTLRSNSKYNVVVSVHKADG-PSQ--IKVSLNGPSYNET-----
AN--LTKDYIDGVYDNAB-YABRFMERNEGHIVDIHDFSLGSSP------HVRKHF
                                                                                                                                                                                                                     -----KOIELP--PMSTONVEFEVPKLATGNYNLSAEGVSGVVFKNSTKLNYADKK
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%; Pred. No. 2.9e-94;
293; Mismatches 541; Indels 182;
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                                                 LYDYYDTERKATEYY--QVKSSLCDICEGADCGEGCK
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                                                                                       ---EKKPSFKVTPTVKDTPNQLLIVD--VCAEYVPLEDADKDKDSNMAVMEIALPSGFVG
                                                                                                                                         RSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSF-----SGPGRSGMALMEVNILLSGFMV
                                                                                                                                                                      GSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDS-------WQPRSLDIEVAAYALL
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RESULT 10
GONFY7
ID QONFY7; Q9VLY8;
AC Q9NFV7; Q9VLY8;
DT 01-CCT-2000 (TTEMBLrel. 15, Created)
DT 01-CCT-2000 (TTEMBLrel. 15, Last sequence update)
DT 01-CCT-2000 (TTEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TTEMBLrel. 23, Last annotation update)
DT 01-MAR-2010 (GH01829p).
GN TEP1 OR TEP2 OR CG7052 OR CG18589.
GN TEP1I OR TEP2 OR CG7052 OR CG18589.
CG NCG18591 (GH01829p).
GN TEP1I OR TEP2 OR CG7052 OR CG18592.
CO ENARYOTA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CO Ephydroidea; Drosophilade;
CO Ephydroidea; Drosophilade; Drosophila.
CO NCBI_TAXID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeifer B.D.,
RA Ballew R.M., Basu A., Bascendale J., Bayzaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kather C., Kravitz S.K.Ip D. Lai Z.,
Lin X., Mattel B., McIntosh T.C., McIntosh 
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Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Holdward C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

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"Sequencing of Drosophila melanogaster genome.";

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                                                                                                                                                                Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubbin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00207; A2M; 1
Pfam; PF01835; A2M_N;
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HSSP; P01024; 1C3D
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EMBL; AE003618;
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; IPR001599; MacrogloblnA2
; IPR000215; Serpin.
IVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLGMFMNSFAVF--QECGLWVLTD
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                                                                                VPKATIYVYYVVNN-DLQFEEKTIDFEKEFSNSIDVS-APTNAKPSEEVKLRIK-TDADS
                                                                                                                                                                                      NTKKPRLGEQVSFDVVSIEDLPYFVYTIVARGNVILSDYVDVPDGQKTYTV-KFTPTFSM
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       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                         Drosophila melanogaster (Fruit 1 Eukaryota; Metazoa; Arthropoda;
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     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Honderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burla K.C., Basu A., Baxendale J., Bayraktargolu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargolu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerblos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebblos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA Goldek R., Gong F., Gorrell J.H., Gu Z., Glanr P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Merkulbov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Mixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H.,
RA Shue B.C., Stdein-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Sun E.,
RA Shen S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Globs R.A., Zhong F.N., Zhong W., Zhang S., Zhu X., Smith H.O.,
RA Schence 287:2185-2195(2000).
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RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Fistan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfetfor C.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
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MEDLINE=20196006; PubMed=10731132;
                              SEQUENCE FROM N
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SEQUENCE FROM N.A.
       Celniker
       S.E.,
       Gibbs
     R.A.,
       Rubin G.M., Venter C.J.;
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InterPro; IPR001599; MacTogloblnA2.
InterPro; IPR001599; Serpin.
Pfam; PF00207; A2M; 1.
Pfam; PF00207; A2M; 1.
Pfam; PF01835; A2M; N; 1.
PROSITE; PS00477; ĀLPHA 2 MACROGLOBULIN; 1.
PROSITE; PS00284; SERPIN; 1.
SEQUENCE 1399 AA; 155783 MW; 3D8B7DF91F
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                                                                                                                                                                                                                                                                                FVGLLGVDQSVLLLKSGNDLSQDDIFNSLNIYQTS---TPWNNGYGRYPGQTSGLVTLTN
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                                                                                                IW-LDTNMGYRIYQEFEVT--VPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIF
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Iwaki D., Kawabata S., Miura Y., Kato A., Armstrong P. Quigley J.P., Nielsen K.L., Dolmer K., Sottrup-Jensen "Molecular cloning of Limulus alpha-2-macroglobulin.";
Eur. J. Biochem. 242:822-831(1996).
EMBL; D83196; BAA19844.1; -.
HSSP; D01024; 1C3D.
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Bukaryota; Metazoa; Arthropoda;

Limulidae; Limulus.

MCBI TaxID=51645;
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InterPro;
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Matches 44S
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Pfam; PF01835; A2M N; 1.
PROSITE; PS00477; ĀLPHA 2 MACROGLOBULIN;
PROSITE; PS00018; EF HAND; 1.
SEQUENCE 1507 AA; 168490 MW; 8EF4013.
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VISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIE
                                                                                             ISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMNSKHLNG
AQFELALPDEPTYGMWRIKGNIEDTEIYENFEVKEYVLPKFEVKITPPSYLLTNADSITW
                                                CISEETGLGVSEA-ATVKGFQFFFVSFTLFYSVIRGEKVPIIVTVFNYLSECLFIKLSLE
                                                                                                                                                                                                                                           VFIQTDKALYKPKQEVKFRIVTLFSDFK--PYKTSLNILIKDPKSNLIQQWLSQQSDLGV
                                                                                                                                             STNYLDSITAFDEAGLVVISDMELETRPCKPSGFEDGGRPCPQYDVAFAAPQAANRIGGG
                                                                                                                                                                    LGMFMNSFAVFQECGLWVLTDANL-----TKDYIDGVYDNAEYAERFMEENEGHIV---
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Q9ULD7;
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01-MAR-2003
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA1283 (Fragment).
KIAA1283.
                                         InterPro;
InterPro;
InterPro;
 Pfam;
Pfam;
Pfam;
SMART;
                                                                         EMBL;
                                                                                                                  MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N.,
"Prediction of the coding sequences of unidentified human of
The complete sequences of 100 new cDNA clones from brain with
                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                               SSUE-Brain
                                                                                             large proteins in vitro."; Res. 6:337-345(1999).
erPro; IPR002890; AZM_N.
srPro; IPR002350; kazal.
srPro; IPR001599; MacrogloblnA2.
n; PF00207; AZM; 1.
n; PF00835; AZM_N; 1.
n; PF00855; AZM_N; 1.
n; PF00850; Kazal; 1.
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P01024; 1C3D.
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Y 664 FMEENEGHIVDIHDFSLGSSPHVRKHFPETWIWLDTNMGYRIYQ-EFEVTVPD 715 1	Matches 49 Matches 49 Matches 49 Matches 49 Matches 49 117 117 236 237 238 330 344 445 574 660	R PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1. W Hypothetical protein.
RESULT 14 Q81ZJ3 PRELIMINARY; PRT; 1885 AA. ID Q81ZJ3; AC Q81ZJ3; DT 01-MAR-2003 (TrEMBLrel. 23, Created) DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) OS Alpha-2 macroglobulin family protein VIP. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606;	Db 881 CLANITAXALAYGDTWCCRDGRSSKHPEENHADRRVPLOTORNARSOWNORMS (1) 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	X

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SEQUENCE FROM N.A.
Li Z., Wu X., Engvall E.;
"Cloning and expression o
member.";
"Cloning and expression o
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                    774
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                   SITSWVGEAVALSTSQGLGI-AEPSLLKTFKPFFVDFMLPALIIRGEQVKIPLSVYNYMG
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RESULT 15

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AC Q60486;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha-macroglobulin precursor:
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"Cloning and sequencing of cDNa encoding plasma
and murinoglobulin from guinea pig: Implications
evolution of alpha-macroglobulin family.";
J. Biochem. 120:1167-1175 (1996).
EMBL, D84338; BAL12316.1; -.
EMBL, D84338; BAL2316.1; -.
HSSP; P01023; 1BV8.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS00477; ALPHA 2 MACROGLOBULIN;
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1
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ITITASEANY-----HSNATTDENGLVQFSINTTNMIGTSLNIQVKHKDSTNCYDYQWLL
                                                                                                                                                                                VVITVTQRNYTEYWSGSNSGNQKMEAVQ-KINYTVPQSGTFKIEFPILEDSS----ELQL
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                                                 LVFYYVIMAKGGIVQSGTYVLSVEQGNTKGHFSVSVPVESDLAPVARVLIYAILPSGEII
                                                                           L--SYMVVSRGQLVAVG-----KQNST----MFSLTPENSWTPKACVIVYYIEDDGEII
                                                                                                    EANEGASHTANAVFSL----SRSFVHLEPQLGKLPCHQTQTFKA----HYILKG-QELKE
                                                                                                                              KAYFLGSKSSMAVHSLFKSPSKTYIQLKT-----RDENIKVGSPFELVVSGNKRLKE
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Search completed: January 15, 2004, 18:14:03 Job time : 64 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB Maximum DB Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US10020095/runat 15012004_0.1-LOODECL=0 -LOODEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-USER=US10020095 @CGN 1 14337 @runat 15012004 163822 18713 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=20 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6 Run Post-processing: Minimum Match 0%
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Listing first 45 summaries Database Total number of hits satisfying Searched: Scoring table: Sequence: OM protein - nucleic search, using frame_plus_p2n model Perfect score: Title: / FGAPEXT=7 seq length: 0
seq length: 2000000000 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext January 17, 2004, 00:12:55; Search time 5629 Seconds (without alignments) 6165.712 Million cell updates/sec US-10-020-095-4 7348 22781392 seqs, 12152238056 residues BLOSUM62 1 MQGPPLLTAAHLLCVCTAAL......HSSVIFIFCFKLLYFMELWL 1428 em_htc:*
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus sequence. AK029247 AK029247.1 GI:26081244 AK029247

AK029247

AK029247

Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831440KI7 product:weakly similar to alpha-2-macroglobulin (fragments) [Limulus polyphemus], full insert Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Please visit our web site for further details.
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Shibata, K.,
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Itoh, M.,

Aizawa, K.,

Nagaoka, S.,

Sasaki, N.,

Carninci, P.,

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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                              sequence.
AK036799
AK036799.1
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihari, C., Momra, K., Numazaki, R., Ohno, M., Obsato, N., Nakamura, M., Nishi, K., Nomra, K., Numazaki, R., Ohno, M., Obsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiragawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gs.c.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                        prepare mouse tissues.
Please visit our web site for further
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                                  URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_sTage="adult"
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weakly similar to alpha-2-macroglobulin (fragments)
[Limulus polyphemus] (PIR|A36260, evidence: FASTY,
51.8*ID, 76.7*length, match=168)"
4707. .4712
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/strain="C57BL/6J"
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                                                   gArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLy 1274
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NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettem
Madan, Stephanie Rodrigues, Amy Sanchez and Michell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (13-JAN-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIMI at: http://image.linl.gov Series: IRAK Plate: 94 Row: b Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: frame shifted.
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BC044072
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1 (bases 1 to 4641)
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                                                                              IleAsn---GlySerAlaAsnPheSerPhe----
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/clone="IMAGE:4681494"
/tissue type="Embryo, stage 31
/clone_Tib="NICHD_XGC_Emb4"
/lab_host="DHIOB"
/note="Vector: pCMV-SPORT6"
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CCAGTCAATGATTTTGGAAATTATGATTATCGGATTCAGGAAGCTGAGGATCACTGTCCA 2007
                                                                                                                                                                                                                                                                                                                     GTCTCCATCAACTCAGCTCAGTGTTGACGTCTCTCGACTCTTCGAGTTCTGACCTAC
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                                                               AGTGTGGTGTTAATGAAACCTGACCAAGAACTGACGGCCGACAAGATTCGGGGACTCTTC
                                                                                           SerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnVal------
                                                                                                                            TCCCTACAAGTTCAGGCAGCT---GCCGGGTCTCTCTGTGGCCTGAGAGTGGTGGATAAG
                                                                                                                                                       SerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAspLys
                                                                                                                                                                                           TITAGGAATAAGGTGTCAGTTGGCTTCTCCCCAGATGAAGTTCTACCAGGATCAGATGTT 1830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerLysSerSerMetAlaValHisSerLeu------PheLysSerProSerLysThr 466
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                               ------ValHisGluLeuGlu------
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	905 GlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGln 924 	885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904 :::	н :	AAGCCACTACTGGTGCAGCCAGGGGGAGTCCTGGAAGAAAAAGCTCACAGTTCTCTGCTC		839	ArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSer	803 GlyHisGlmGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIle 822	783 IleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThr 802 	763 GluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysVal 782 ::: ::: 2540 TCATTCGCTCTCAAGGCCACTGTCTTTAACTACCTGAAGCAGTGTATAAAGGTTCAGACA 2599	743 GlnAlapheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArgGlyGlu 762 ::: :::	723 ThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGluLeu 742	703 TyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAla 722	686ValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMetGly 702 :::: ::::	675 IleHisAspPheSerLeuGlySerSerProHis	657AsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHisIleValAsp 674 ::: ::: ::::: 2188 GCCAGGGCTACCAGGACCTCCAGGACCTACTGGAGACCGAATGATTG-CATTTGCTTCCC 2246	640 ValLeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAsp 656 :::::	620 GlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrp 639 :::::::: :::	616LeuTyrAsnThr 619 2008 TTCCGACCCTTTCTTCCTTGGCGACCATTCAATAGAATTTCTAGATCCATTATATATCCC 2067
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1256 ArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLys 1274	1236 ATATIECYSGJNIHEWASNVALVALTYKASNVALTYSATIASETGIYSETSETATGATGATG 1255	::: ::: ::::::	::: 3935 AAGACTGGATTCCATCAACAGTTCCATGTGGATCAAAATAACCGGCTCCTGCTACAGAAA 3994 1216 SerProLeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPhe 1235	3875 GCTAAGTATGCCGAGGCCACATTCACTGACAAGGAGATGTAACAGTCACAGTCACATTCC 3934 1212 ProSerSerPro 1215	3815 CAAAATCCATATGGGGGATTCTCTTCTACTCAGGACACGGTTGTAGCTCTACAGGCTCTT 3874 1192 SerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGly 1211	1172 ArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLySAlaLeu 1191	1154LeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeuSerArgGln 1171	1134 SerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAlaLeuLeuSerHisPhe 1153	1118 GluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeuSerAsp 1133	1099 ValGlySerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGln 1117	1081ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSer 1098		GAAA	GlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGlyAsnLysSer	1005 IleAspGlnAsnValleuHisArgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsn 1024 :::::	985 SerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAsp 1004	965 LeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGly 984	945 LeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGlu 964 :::	925 AsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGln 944 ::: :::

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REFERENCE
AUTHORS
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                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 941)
                                                                                              cgi-bin/cluster.cgi?seq=CSOBAI029ZD07_CS02740_1&cluster=3578.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAI029ZD07_CS02740_1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081YB18"
                                                          organism="Homo sapiens"
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                                                                           ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr
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                                                            ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA
                                                                                                                                          GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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cgi-bin/cluster.cgi?seq=CSODIOsDA09QP1&cluster=3578.f. Contar
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
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   AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla
                                                         AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly
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/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
3 238 c 236 g 293 t 75 others
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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1 (bases 1 to 4667)
Strausberg,R.
Direct Submission
                                                Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mus musculus, murinoglobulin
                                                                                                     Mus musculus (house mouse)
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                                                   Chordata;
Rodentia;
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                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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one IMAGE:5097177,
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Best Local Similarity:
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ORIGIN
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Series: IRAK Plate: 99 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6678965
This clone has the following problem: frame shifted:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: niso_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.
                                                                           ValThrAlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu
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ACAGCTTCCTTGGTATCTCAATCAGGAAGGAAAAAACCTGTTCGATGAGCTGGTGCTTGAC
                                     ThrValSerValLeuGluAlaGluGly-----
                                                                                                              GluHisCysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeu
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1126 c 1046 g 1149 t
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/clone_lib="NCI_CGAP_Li9"
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/clone="IMAGE:5097177"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTCAATTCTCAGCTAGAC---AACAATGGCTGCAGTACACAAGAAGTGAACATCACT
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                                                       AsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSer
                                                                                                                                                                                                         PheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArg 385
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                                                                                                                              ArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySer
                                                                                                                                                                       TTCTTTGTGAAAGTCCGCCTAGTGGATATCAAGGGAGACCCTATCCCAAATGAGAAA----
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                                                                                              CTTCATCAAAGCACAAGAACTTAGCTATACCAGTGCTACTACCACTGAT 1266
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669 uGlyHisTleValAspIleHisAspPheSerLeuGlySerSerProHisValArgLysHi 689	651IleAsp-GlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGluGluAsnGl 669		641Leu: 641 2020 GCTGAGAAGCACACAAACTTAGTACCACATGGAACTGAGAAGGATGTCTATAGATATGTG 2079 642 ThrAspAlaAsnLeuThrLys	AlaValPheTrpVal :::::	1867 GCTGTGGACCAGAGTGTGCCTACTCCCTGAAACCCGAGTCTGAGCTCTCCCCTTCC 1920 611 ValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPhe 630	::: :::	551 ValGlnLeuValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluPro 570 :::::: :::::::::::::::::::::::::::::	ValileValTyrTyrileGluAspAspGlyGluIleIleSerAspValLeuLysIlePro :::::::	1570 CHASSANGCAICAICCAGACIGGAACCCAIACICACCAGGIIGGAGCCAGGAGAAGCICCA 1629 517PheSerLeuThrProGluAsnSerTrpThrProLysalaCys 530 11630 GTAAAAGGAAAATTTGCCTTGGAGATCCCTGTGGAGGTTTAGATGGTTGGT	ArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMet	ValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetValValSer	ArgAspGluAsnIleLysValGlySerProPheGluLeu	AlaValHisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr	446	426 GlyThrPheLysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAla 445
Oy 1032 rgVallleHisSerGluLeuGlnGlyGlyAsnLysSerProValThrEuThrAlaTyrI 1052 Oy 1032 rgVallleHisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrI 1052 ::: :::::: :::::	992 3234	974 heSerAlaPheGlyAsnTyrAspProSerGlySerThrTTpLeuSerAlaPheV			894 rgValGlnIl 2934 GAGCCCATTT	Db 2823 AAGGAATCAAGCAAGAGCATACCTTCAGCTCACTGTTCTGTGCATCAGATGCTGAGATAT 2882 Qy 874 lnserThrLeuscrpheserPheserPheproproasmThrValThrGlyserGlua 894	Db 2763 GGCCACAGTTCCTGAAACTGGGAGAAAGGACAGTAGTCAAAGTCCTGATAGTTGAGCCTG 2822 Oy 854	829 uIleProIleThrValThrAlaLeuSerProThrAlaSerAspAl :::	Qy 809 uValProSerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGl 829 :::	Qy 789 sPheAsplieLeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLe 809	Qy 769 rilePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLy 789 ::: Db 2541 TGTGATGAACTATCTCCCCACAAGCATGCAGATGAGTGTGCAGCTGGAAGCCTCTCCTGA 2600	Qy 749 ellePheLeuAsnLeuProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleTh 769 ::: :::::: :::	Qy 729 uAspLeuGlyLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGlnProPhePh 749	Qy 709 eGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerg1 729	N

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CACTGGCCTTCTCCTTCATCATTCAACAAGATATCCCAGTAAGGAACCTGCAGCCTGCCA
                                                   lnPheCysValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaS
                                                                                                                           GCAGAACAGAAGTGAGCAACAATGTCTTAATATTTTGGATCAGGTGACCAATCAGA
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                                                                                                                                                                    -GluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSerValAsnGluThrG
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BUS17328
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Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; I
Eukaryota, Metazoa; Chrimates; Catarrhini; Hominidae;
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM14090 row: p column: 10
High quality sequence stop: 663.
Location/Qualifiers
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Tissue Procurement: ATCC
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                                                                LysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAlaLeu
                                                                                                                                 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
                                                                                                                                                                                                     GAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTTCAGACAATTATACTCTA
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
Average insert size 2.1 kb. "
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                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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UI-H-COO-arh-c-08-0-UI.81 NCI_CGAP_Sub9 Homo sapiens
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                Seq primer: M13 FORWARD POLYA=Yes.
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carcinoma, Bladder carrinoma, Brain oligodenroga;
NCI CGAP Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TAGC, TAAGC, ATGG, AGACA, ATCAC. For additional information, contact: Bento Soares, bento-soares@ulowa.edu
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TAG_TISSUE=Cervical Adenosquamous Carcinoma
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Matches:
Conservative:
Mismatches:

Indels: Gaps:

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US-10-020-095-4 (1-1428) x BQ028040 (1-667) 545 GAGATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGT 665 GCGGAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTC TyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrp TyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysPro ThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeu GluIleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSer 119 PheGluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAsp AlaGluLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyVal LeuSerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisPro TTTGAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGAT 546 606 186 246 199 159 426 486 306 366 99 79

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL576908 1201 bp mRNA linear AL576908 Homo sapiens PLACENTA COT 25-NORMALIZED ECLONE CSODIO81YB18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                cgi-bin/cluster.cgi?seq=CSODIO81DAO9NP1&cluster=3578.f. C
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSODIO81DAO9NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="FLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSDORT 6 vector. Library was normalized
a 248 c 224 g 321 t 64 others
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi, ... Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomara, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramtsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1495)
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                                                                                                                                                                                                                                                                               Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in R. Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcom Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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LysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeu 1266
                                                                          AATGTTTCTGCGCATGGCTCGGGATTTGCTATTTGCCAGCTTAATGTTGACTATAACGTG
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VTGFGIPRSIHFRIDSQNLFLLHQEELHALDFITVNVSAHGSGFAIQQLNVDYNVKGS
GSSKRRRSTENQEVFDLDVIVNNEDDISHLNLNVCTSHLGSERTGMVLMEVNLLSGFS
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/clone_Tib="RIKEN full-length enriched
/dev_stage="3 days neonate"
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/db_xref="FANTOM_DB:A630065N19"
/db_xref="taxon:10090"
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BR 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Meb: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
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                                                                                                                                                                                             http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIAI021ZB10QP1&cluster=3578.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI021ZB10QP1.
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1 (bases 1 to 978)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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sapiens
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor \(\)
sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                   clone="CSODI081YB18"
                                                                                                                    db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Tissue Procurement: Gilbert Smith,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                           LysSerAsnG1yG1uPheTrpAspProG1yArgVa1I1eHisSerG1uLeuG1nG1yG1y
                                                   TATATAGATATTGATCAGGATGTGTTACACAGAACATATACTTGGCTTAATGCACATAAG
                                                                TyrileAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGln 1021
                                                                                                                TCTTCTGGGAGCACTTGGCAGCATTTGTTTTAAGATGCTTTCTGGAAGCTGATTAC
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
179 c 202 g 227 t
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/dev_stage="10" months, virgin"
/lab_host="DH10B"
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/clone="IMAGE:4457172"
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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979.50
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77.82%
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s musculus cDNA clone IMAGE:4457172 5',
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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtaine
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Butheria; Primates; Catarrhini; Hom
1 (bases 1 to 638)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-H-FG1-bgj-l-22-0-UI.s1 NCI CGAP FG1 Hc
UI-H-FG1-bgj-l-22-0-UI 3', mRNA sequence.
BU624356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
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/organism="Homo sapiens"

/mol types"mRNA"

/db_xref="taxon:9606"

/clome="UI-H-FG1-bgj-1-22-0-UI"

/tissue_type="Cell lines"

/dev stage="Addult"

/lab_host="DH10B (Life Technologies)"

/clome lib="NCI CGAP FG1"

/note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)

with a modified polylinker; Site_1: EcoR I; Site_2: Not
                                                                                                                                                                                                                                                      ocation/Qualifiers
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RESULT 14
BB613975
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Best Local Similarity:
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BB613975 648 bp mRNA linear EST BB613975 RIKEN full-length enriched, 0 day neonate head
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ=CGGTCACTC"
139 c 109 g 187 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Pujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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1 (bases 1 to 648)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished

Contact: Yoshihide Hayashizaki
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BB613975
BB613975.1 GI:16454440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki,Y
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
                                                                                                                                                                                                                                                                                                                   /tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="4832419I01"
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634 bp mRNA linear EST 16-OCT-1997 zv93f07.rl Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:767365 5's similar to TR:G534873 G534873 ALPHA-2-MACROGLOBULIN.;, mRNA
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                                                                                                                                                                                                                                            LysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly 1041
                                                                                                                            TyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGlu 1076
                                                                                                                                                                                                                                                                                                 TyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGln 1021
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Best Score: Pred. No.: Alignment BASE COUNT

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Query Match:
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Email: estGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washlu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) f. Seq primer: -28ml3 rev2 ET from Amersham
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1. (bases 1 to 634)
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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SerLeuSerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeu 1334
                                                                                                   GlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIle 1314
                                                                                                                                                                                                       AspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGlyArgSer
                                                                                                                                                                                                                                                                                                          ArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLys
                                                                                                                                                                         GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGT
                                                                                                                                                                                                                                                                               CGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Soares NhHMPu S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and se circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Pooled human melanocyte,
pregnant uterus"
/lab_host="DH10B"
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db_xref="taxon:9606"
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Indels:
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GluLeuTrpLeu 1428 AACTTTGGCTG 522	1415 IlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428 	1415 481	B 8
395 GlyCysArgProCysGluAspGlyAlaSerGlySerHisHisHisSerSerValllePhe 1414 	1395 GlyCysArgProCysGluAspGlyAlaSerGlySerHisHisSerSerValllePhe	1395 421	P 6
1375 ValargSerTyrasnSerGluValLysLeuSerSerCysAspLeuCysSerAspValGln 1394 	ValargSerTyrAsnSerGluValLysLeui 	1375 361	유 상
.355 SerAsmThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAla 1374 	SerAsnThrGlnAspAlaSerValSerIle	1355 301	B &
1335 AspSerValAsnGluThrGlnPheCysValAsnTleProAlaValArgAsnPheLysVal 1354 	335 AspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysVal	1335 241	B 8

Search completed: January 17, 2004, 02:52:00 Job time : 5723 secs

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Result
No.
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Perfect score:
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      7331
7326.5
7326.5
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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Match
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7348
1 MQGPPLLTAAHLLCVCTAAL.....HSSVIFIFCFKLLYFWELWL 1428
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(without alignments)
4197.436 Million cell updates/sec
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      ABB82165
ABB82167
AAO19372
AAE32013
ABB82166
ABB82168
AAO19373
AAB12127
                                                                                                                                                                                   AAE32012
                                                                                                                                                                                                                                                                                             SUMMARIES
Human r150 protein
Human CD109 K1 pro
Human CD109 K1-H7
Human platelet all
Human r150 protein
Human CD109 K1 var
Human CD109 K1 var
Human Dlatelet all
Hydrophobic domain
                                                                                                                                                                                                                             Description
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Drosophila melanog	ABB62893	22	798	15.0	1099.5
	ABB67122	22	753	15.0	
	ABU52373	24	1436	15.1	1109.5
Human GPCR related	ABU52372	24	1411	15.7	1157
Human protease and	AAB74689	22	248	•	1173.5
Human cancer assoc	AAB43949	21	1285	17.1	1255
Drosophila melanog	ABB62921	22	1413	17.7	1299.5
Novel human diagno	ABG28005	22	1542	17.9	1315.5
Larval viability a	ABG70020	23	1760	18.1	1328.5
Drosophila melanog	ABB63367	22	1760	18.1	1328.5
Alpha-1 proteinase	ABB99092	23	281	18.1	1329.5
Novel human diagno	ABG21224	22	1475	18.4	1352.5
	ABB09519	23	1479	18.7	1376.5
Novel human diagno	ABG28006	22	1487	19.0	1396.5
Drosophila melanog	ABB71908	22	1425	19.1	1406
alpha-	ABG61768	23	1492	19.2	1413.5
Human alpha-2-macr	ABG76898	23	1492	19.3	1418.5
Human alpha-2 macr	AAR11749	12	1484	19.4	1425
Recombinant human	AAR11334	12	1474	19.4	1428.5
Drosophila melanog	ABB66669	22	1203	19.5	1430
Human alpha2 macro	AAU81018	23	1451	19.6	1437
A human alpha-2 ma	AAG63548	22	1508	19.6	1437.5
Human alpha2 macro	AAU81017	23	1474	19.6	1440
Human alpha 2 macr	AAU74798	23	1474	19.6	1440
Hypoxia-regulated	ABP65218	23	1474	19.6	1440
Human alpha-2 macr	AAB50673	22	1474	19.6	1440
	AAY97157	21	1474	19.6	1441
	ABB11581	22	352	21.7	1592
Human polypeptide	ABB90069	23	336	22.2	1628.5
elegans alpha-	AAB50677	22	1519	25.2	1850
	AAB50676	22	1508	25.2	m
Human blood cell s	AAE32018	24	1445	38.9	2860.5
CD109 K15	ABB82170	23	1067	•	5461
CD109 K15	ABB82169	23	1067	٠	•
r150 protei	AAE32015	24	1399	96.2	7068.5
Human blood cell s	AAE32014	24	1382	96.4	7081

ALIGNMENTS

AAE32012 standard; Protein; 1428 AA

AAE32012;

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RESULT 1
AAB32012
ID AAB3
XX AAB32012
AC AAB3
XX AAB3
XX Huma
DE Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
CX Homc
CX Homc
XX Homc
CX Homc
XX Hom
XX Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal;
                                                  24-APR-2001; 2001US-285713P.
14-FEB-2002; 2002US-356163P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                 24-APR-2002; 2002WO-CA00560
                                                                                                                                                                                                                                                                                            31-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "GPI anchor cleavage site"
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 94-99; 127pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-093100/08.
DB; AAD49434.
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                                                 ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY
                                                                                                             SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDG
                                                                                                                                                                                                                                                                                                                         TVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVG
                                                                                                                                                                                                                                                                                                                                                                                                                KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQXINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWL
                                                                                                                                                                                                      SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYY1EDDG
                                                                                                                                                                                                                                                                                             TVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVG
                                                                                                                                                                                                                                                                                                                                                                                      KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
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Pred. No. 0;
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ARBEAT A
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 1427; Conserv
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CD109 K1
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                                                                                                                                                                  or their antisense nucleotide sequence treating these conditions. The present CD109 K1-H7 sequence.
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated nucleic acid molecules encoding CD10: polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variant; CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, (family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
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                                                                                                                                       Sequence
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The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or neonatel alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova encoded protein.
                                                                                                                                                                                                                                    thrombocytopenia
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                  WPI; 2003-093100/08
N-PSDB; AAD49435.
                                                                         24-APR-2001;
14-FEB-2002;
                                                                                                                                                                                                                  Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal;
                                          Philip
                                                                                                 24-APR-2002;
                                                                                                                                                                                                                                           Human r150
                                                                                                                                                                                                                                                                           AAE32013;
                                                                                                                                                                                                                                                                                          AAE32013 standard; Protein; 1445
Novel transforming growth factor (TGF)-beta 1 binding reagent which
                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                          protein #2.
                                                                         2001US-285713P.
2002US-356163P.
                                                                                                  2002WO-CA00560.
                                                                                                                                                                                                                                                           (first
                                                                                                                                                                  Location/Qualifiers 703
                                                                                                                                                 note= "Encoded by TNC"
                                                                                                                                                          label= Ser,
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comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer -
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Claim 1; Page 103-109; 127pp; English

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein.

Sequence 1445 AA;

Similarity

Score Pred.

7318.5; No. 0;

DB

24;

Length

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Matches 1426; Conservative
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                                                        EIISDVLKI PVQLVFKNKIKLYWSKVKABPSEKVSLRISVTQPDSIVGIVAVDKSVNLMV
                                                                                                                                                                                                                                         SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDG
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                                                                                                                            ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY
                                                                                                                                                                                                                            SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDG
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                                                                                                              ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY
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KW CD10
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               07-MAR-2001; 2001US-273814P
                                                                                                                                                                                                    Human CD109 K1 variant protein.
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                                        07-MAR-2002; 2002WO-CA00292
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for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired or itvation of the coagulation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocytopenia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for
                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated nucleic acid molecules encoding CD10 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-TD109 K15 or their variant CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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                                                              The present sequence represents the human
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CD109; alpha2 macroglobulin; thioester; cerebroprotective; card immunosuppressive; haemostatic; anticoagulant; thrombolytic; hu cardiovascular; vasotropic; gene therapy; CD109 KI-H7; variant.
                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                07-MAR-2001; 2001US-273814P
                                                                                                                                                                                                                           07-MAR-2002; 2002WO-CA00292
                                                                                                                                                                                                                                                                                            Human CD109 K1-H7 variant protein.
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New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombostopenia, autoimmune diseases, or organ or bone marrow transplantation -

Claim 21; Fig 3b; 156pp; English.

for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired activation of the coagulation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human CD109 K1-H7 variant sequence. The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1. CD109 K1. CD109 K15 or their variants. CD109 is a novel member of the alphaz macroglobulin (alphazM)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful

Sequence 1445 Æ

망 ð 맑 8 Query Match Best Local Simi Matches 1426; 61 61 Similarity MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST Conservative 99.6%; Score 7317.5; Pred. No. 0; 1; Mismatches В ۲, 23; Indels Length 1445 17; Gaps 60 60

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The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that disringuishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets,—2, post-transfusion purpura, post-transfusion platelets refractoriness or meonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Govb encoded protein.
Sequence
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New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune

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                                                                                                                            GDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQG
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AAB12127 standard; Protein; 1445

AAB12127;

02-FEB-2001 (first entry)

Hydrophobic domain protein isolated from HT-1080

Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; prophylaxis; signal receptor; ion channel; transporter; immunostimulant immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

sapiens.

WO200029448-A2

25-MAY-2000

17-NOV-1999; 99WO-JP06412

17-NOV-1998; 22-DEC-1998; 16-MAR-1999; 27-APR-1999; 19-MAY-1999; 98JP-0326255. 98JP-0364315. 99JP-0069811. 99JP-0119299. 99JP-0138169.

(SAGA) (PROT-) SAGAMI CHEM RES PROTEGENE INC.

Kato Kimura H

2000-387753/33. DB; AAA60199, AAA62010

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Proteins comprising hydrophobic regions, such as secretory and me proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic. secretory and membrane

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimune disease, Alzheimer's disease, Parkinson's
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                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer
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N-PSDB; AAD49437.
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The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules (CD104) and (CD105) KI. (CD105) Is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (CD105) polypeptides can be compressed to rise and continuous activation activation of polypeptides or impaired activation of Tlymphocytes (CD105) polypeptides or impaired activation of Tlymphocytes (CD105) polypeptides or impaired activation of Tlymphocytes (CD105) polypeptides (CD105) polyp
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                                                                                                                                                                                                                                                      Sequence
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Best Local S
Matches 1061
                                                                                                                                                                                                                                                                           for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired activation of the coagulation and/or fibrinolytic systems, or impaired or increased inmune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombosytopenia, thrombosythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated nucleic acid molecules encoding CD10; polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variant; CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, (family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombostopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 K15; variant.
                                                                                                                                                                                                                              Sequence
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AAE32018 standard; Protein; 1445 B

(first entry)

Human blood cell surface antigen, CD109 #2

Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal;

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Note: This sequence is stated to be encoded by human CD109 DNA shown in figure 17 of the specification, but this does not appear to be the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                 KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKINY
                                                            AVMASSAGLSGTLALSSPGPVGILTTVTGSVTGISAAVSTAVPPLGHATIIGPPATTTVL
                                                                                     NVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTTVL
                                                                                                             MASLHLAGTITALTTTGLPVLGAVTLTPLPLSPTGLLLAITLTPLIAGSAAPSPAAGGML
            LPSLAPTATVLVTAAAGAGLTLGGAAAAVVITVTGAATTGTTSGSASGAGLMGAVGLIAT
                                                                                                                                      MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDBEMK
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                                                                                                                                                              SGGSALGVISLTPGLSSHPILGATSIGVGVAAGTTTGSPGVSGTVLPLPGVTLGTPLTCS
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                                                                                                                                                                                         YNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNL
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                                                                                  LSGPMVPSGAISLSGTVLLVGTAHGLLALTLASVAGTGPCVAIPAVAAPLVSATGAASVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) a human unc-HS1 cDNA, useful in yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact with the human unc-5C protein -
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   ANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDY
                                                              GTITAKYTYGKPVKGDVTLTF-LPLSFW--
                                                                                                                                                          FIOTDRAIYRPASLVRYRAIVVKSDLKPYVGNATIKIFDPSRNLISQTIGVTLDRGVYSG
                                                                                                                                                                          FIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLGVISK
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                                                                                                                                                                                                                                                                             VCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVL
                                VFVDAKYTYGKGVAGKAKVSLELPWHRWHAMVPTIIDENGVKKEEELMVERTVKLNRQGE
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                                                                                                                                                                      SAQKKVEKLKESRAYMFQARFVDIETTSYAVLSYLAQNQTSESLSIIRWLVSQRNELGGF
                                                                                                                                                                                                   VSSE--SKLSDS-----WOPRSLDIEVAAYALLSHFLOFOTSEGIPIMRWLSRORNSLGGF 1178
                                                                                                                                                                                                                                 ENGKAVTYLEKHLDEVSGNAYTMAVVAYALQLAKSKQAGKAFENLKKHKIVEKSGDVKFA
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                                                                                                                                                                                                                                                                                                                             NVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGG-NKSPVTLTAYIVTSLLGYRKYQPNI 1066
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                                                AVSINANGTGVVFAQLSYSY
                                                                          AVNISANGEGEAICQLNVVYNVKASGSSRRRRSIQNQEAEDLDVAVKENKDDLNHVDLNV
                                                                                                          TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
                                                                                                                                         ASTODTTVALKALSEFAALMNTERTNIQVTV-TGPSSPS-----PLAVVQPM-----
                                                                                                                                                                                                                                                                                             NVISRAVAFLNSQQMESGAFAERGEVHHKDMQGGAQDGGVALTAFVLISIL-----ENGM
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Search Job ti	B & B
Search completed: January 15, 2004, 18:12:20 Job time : 59 secs	1356 CCNYTRPGKSNMALAEIDALSGYRPDAEQVHTLTSIEDLQRVEMEKDDTKMNVYFNPLGG 1415 1340 TQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRP 1398

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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Saunders, Aleister J.
APPLICANT: Sunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
SOCTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1474
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                                                                                                                                                                                                                          GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ-------
                                                                                                                                                                                                                                                                                                                           VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF 1074
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                                                                                                                                                                         GGFSSTODTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                LES-----EFSRGISDNYTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFW---
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                                                                                                                          PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
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US-08-447-411-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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TELEFAX: (703) 413-2220
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-447-411-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/447,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3,
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S. Jefferson Davis Highway, Suite CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1354
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                                                                                                                                                                                                                                                   60 A----ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEIL 115
                                                                                                                                                                                                                                                                                                                                                         1 MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELL-EHCPSQVTVK 59
                                                                                                                                                                                                                                                                                                         MEGMALYLVAALLIGFPGS---SHGALYTLITPAVLRTDTEEQILVEAHGDSTPKSLDIF
                                          IQQWLSQQSDLGVISKTFQLSSHPI-------LGDWSIQVQVN----DQTYY 216
                                                                                                                                             FSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNL 175
                                                                                                                                                                                                   VHDFPRKQKTLFQSRVDMNQAGSMFVT---PTIKVPAKELNKDSKQNQYVVVKVTGPQVA
----FQTPEGIV-----VSSKPVNPSGSIRPYNLPELVSFGTWKAVAKYEHSPEESYT
                                                                                             LEKVVLLSYQSG--FVFIQTDKGIYTPGSPVRYRVFSV--DHNMHRMDKTVIVE-----
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SHORST, REINHARD
,, CARL-WILHELM
                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%; Score 973.5; DB 1; 23.5%; Pred. No. 9.8e-72;
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VAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTER- 1202
                                              QRPYTTALTAYALA----AADRLINDDRVLMAASTGRIRW-----EEYNARTHNIE
                                                                                               SDNYTLALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIE 1143
                                                                                                                                                                                                  ELOGGNKS---PVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRG-----I
                                                                                                                                                                                                                                                N--RASSSWLTAYVVKVLAMASNMVKDISHEIICGGVKWLILNRQQPDGVFKENAPVIHG
                                                                                                                                                                                                                                                                                                  NYDPSGSTWLSAFVLRCFLEADPYI-DIDQNVLHRTYTWL-KGHQKSNGEFWDPGRVIHS 1036
                                                                                                                                                                                                                                                                                                                                                GEONMITMTPSVIATYYLDATGOWENLGVDRRTEAIKQIMTGYAQQMVYKKADHSYAAFT
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US-08-793-126-1
; Sequence 1, Application US/08793126
; Patent No. 5849297
; GENERAL INFORMATION:
APPLICANT: Harrison, Richard Alexander
; APPLICANT: Farries, Charles Timothy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
; NUMBER OF SEQUENCES: 2
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                                        Matches
                                     Best Local Similarity Matches 376; Conserv
                                                                            Query Match
                                                                                                                                                                                                   TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino acids
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United Stat
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 1i
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                                                                                                                                                                                       TYPE: amino acid
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ISMLTGFFPDAEDLKRLSNGVDRYISKFEIDNNMAQKGTVVIYLDKVSHSEDECLHFKIH 1452
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                                                        12.7%; Score 931; DB 2; 23.0%; Pred. No. 3.6e-68;
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  YQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWL-KGHQKSNG 1025
                                              RLKHLIVTPSGCGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLA
                                                                                             -LASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEK---ALSFMRQGYQRELL
                                                                                                                                            AV-RTLDPERLGREGVQKE----DIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDAE
                                                                                                                                                                                           SILLDLTDNRL--QSTLKTLSFSFPPNTV-----TGSER----VQITAIGDVLGPSING-
                                                                                                                                                                                                                                                                                         QQTLLVPSEDGATVLFPIRP--THLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQ
                                                                                                                                                                                                                                                                                                                                       DFFIDLRLPYSVVRNEQVEIRAVLYNY-RQNQELKVRVELLHNPAFCSLATTKR----RH
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TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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RESULT 4
US-09-132-271-1
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Patent No. 6221657
APPLICATION NUMBER: US/08/793
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk-
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harrison, Richard Alexander
APPLICANT: Farries, Charles Timochy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: MA
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                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                    EDLKEPPKNGISTKL-----MNIFLKDSITTWEILAVSMSDKKGI-CVADPFEVTVMQ
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                                                                                                APPLICANT: Farries, Timothy C.
APPLICANT: Harries, Richard A.
APPLICANT: Harrison, Richard A.
TITLE OF INVENTION: Down-Regulation Resistant C3
FILE REFERENCE: 4-30443/A/IMU/PCT
CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
                                   ; TYPE: PRT; ORGANISM: Homo
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 Query Match
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TYPE: PR
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                                                                QQTITIPPKSSLSVPYVIVPLKTGLQEVEVKAAVYHHFISDGVRKSLKVVPEGIRMNKTV
                                                                                                      QQTLLVPSEDGATVLFPIRP--THLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQ
                                                                                                                                                 DFFIDLRLPYSVVRNEQVEIRAVLYNY-RONQELKVRVELLHNPAFCSLATTKR----RH
                                                                                                                                                                               PFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIE--KSDKFDILMTSSEINATGH
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                                                                                                                                                                                                                                                                       ------LDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQ 746
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286; Mismatches 615;
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APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FO
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                         ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb
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APPLICANT:
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                                                                                                                                                              ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park
CITY: New Haven
  COMPUTER: Macintosh Cetris
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
                                                                                                                          COUNTRY: USA
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Mueller, Eileen
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AUTHORS: Fleischer, D.T.
AUTHORS: Hunt, A.
AUTHORS: Wetsel, R.A.
TITLE: Complete cDNA Seque
Patent No. 6355245
TITLE: Complement Pro-C5
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Best Local S
Matches 379
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SEQUENCE CHARACTERISTICS:
LENGTH: 1676 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Haviland, D.L.
AUTHORS: Haviland, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seth A. Fidel.
REGISTION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: AL.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1076-1790
TELEPHONE: (203)776-1790
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APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
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DESCRIPTION: Pro-C5 Polytpeptide
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VOLUME: 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 921; DB 4; I al Similarity 24.0%; Pred. No. 2.5e-67; Score 921; Mismatches 621;
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                                                                                                                                                                                                                                 KYTYGKPV-KGDVTLTFLPLSFWGKKKNI------TKTFKINGSANFSFNDEEM
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                                                                                                                                                                                           RYFYNKVVTEADVYITF-----GIREDLKDDQKEMMQTAMQNTMLINGIAQVTFDSE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEKTLTLPSLP--LNSADEIYELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYK 141
     MEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLK 471
                                       PLFLKPGIPYPIKVQV------KDSLDQLVGGVPVILNAQTIDVNQETSDLDPSKSVTRV
                                                                             TTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI-----TVTQRNYTEYWSGSNSGNQK 411
                                                                                                                                                      KNVMDSSNGLSEYL -- DLSSPGPVEILTTYTESVTGISRNVS-TNVFFKQHDYIIEFFDY
                                                                                                                                                                                                                                                                      YGMWTIKAKYKEDFSTTGTAY - - FEVKEYVLPHFSVSIE - PEYNFIGYKNFKNFEITIKA
                                                                                                                                                                                                                                                                                                                                               PDQSVKVRVYSLNDDLKPAKRETVLTFIDPEGSEVDM-VEBIDHIGIISFPDFKIPSNPR
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                                                                                                                                                                                                         RYGGGFYSTQDTINAIEGLTEYSLLVKQLRLSMDIDVSYKHKGALHNYKMTDKNFLGRPV
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                                                         GNSDYKRIVACASYK-PSREESSSGSSHAVMDISLPTGISANEEDLKALVEGVDQLFTDY 1453
                                                                                                                                                                       AVVQPMAVN---ISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQ-EAFDLDVAVKENK
                                                                                                                                                                                                                                                                                    NPPIYRFWKDNLQHKDSSVPNTGTARM--VETTAYALLTSLNLKDINYVNPVIKWLSEEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMS-----YRNADYSYSVWKG--GSASTWLTAFALRVLGQVNKYVEQNQNSICNSLL 1105
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                                                                                          DDLNHVDLNVÇTSFSGPGR-----SGMALMEVNLLSGFMVPSEAI-SLSETVKKVEYDH 1327
                                                                                                                                  EVL----LNDDLIVSTGFGSGLATVHVTTVVHKTSTSEEVCSFYLKIDTQDIEASHYRGY 1394
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MOLECULE TYPE:
US-08-662-227-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/662,227 FILING DATE: 14-UN-1996
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COUNTRY: US
ZIP: 22202
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STRANDEDNESS: single
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FF-WPYNLPDLVSLGTWRIVAKYEHSPENYTAYFDVRKYVLPSFEVRLOPSEKFFYIDGN
                                                                                                                           VISKTFQLSSHPILGDWSI---QVQVNDQTYYQSFQVSEYVLPKFEVTLQTP---LYCSMN
                                                                                                                                                                                                                                        RISVFIQIDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLG
                                                                                                                                                                                                                                                                                            QTRVDMNPAGGMLVT---PTIEIPAKEVSTDSRQNQYVVVQVTGPQVRLEKVVLLSYQSS 126
                                                                                                                                                                                       --FLFIQTDKGIYTPGSPVLYRVFSMDHNTSKMNKTVIVEFQTPEGILVS---SNSVDLN
                                                                                                                                                                                                                                                                                                                                              NLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127
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1755 S. JEFFERSON DAVIS HIGHWAY
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Matches 361; Conservative 225; Mismatches 672; Indels 276; Gaps 56; Oy 18 AALAVAPGPRFLVTAPGIIRPGGNVTIGVELL-EHCPSQVTVKAELLKTAS 67	TYPE: protein -2 -2; Score 894;	; ITE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear	H: CHA	E/DOCKET NUMBE ICATION INFORM E: 703-413-30	N-199 ATION N F. N E.	FILING DATE: ; FLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/662.227	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/017,947	ZIP: 22202 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible	뷰!!! ' ' ' ' ' ' '	RECUENCES: 39 RECUENCE ADDRESS: RECUENCES: 39 RECUENCES: 39 RECUENCES: 39 RECUENCES: 39	BREDEHO KOCK, N FRITZIN	; Sequence 2, Application US/09017947 ; Patent No. 6303754 ; GENERAL INFORMATION: ; APPLICANT: VOGEL, CARL-WILHELM	RESULT 8 US-09-017-947-2	Qy 1396 CRPCEDGASGSHHHSSVIFIFCFKLLYFME 1425	Qy 1337 VNETQ-FCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQG 1395	Qy 1287 SFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVKKVBYDHGKLNLYLDS 1336	Qy 1233 FGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCT 1286
Q B Q 6	5 & B	ρ	당 성	Qy db	g Qy	Db Qy	QQ dd	D Q	Db	р, Q	D Q	Qy db	B &	D Q	D Qy) p Q	d dd dy
975 ENSIDGSKLNHLITTPSGCGERONMIRWAAPVLATYXLDTTEGWETLGINRRTEAVNOIVT 1034 960 GYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCF-LEADPYIDIDQNVLHRTYTWL- 1017	S VVPEGVQKSIVTIVKLDPRAKGVGGTQLEVIKARKLDDRVPDTBIETKIIIQGDPVAQII 5 GPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQ	851 VKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITAIGDVL 904	793 LMTSSEINATGHQQTLLVPSEDGATYLFPIRPTHLGEIPITVTALSPTASDAVTQMIL 850	733 IGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDI 792 : : : : : : : : : : : : : :	679 SLGSSPHVRKHPPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLG 732	650GHIVDIHDF 678 687 MGYTCEKRAKYIQEGDÄCKAAFLECCRYIKGVRDENQRESELFLARDDNEDGFIADSDII 746	639 WVLTDANL-TKD	579 SVTQPDSIVGIVAVDKSVNLMVASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGL 638 	527 PKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRI 578	479 VGSPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWT 526	419 NYTVPOSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIK 478	359 VLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQENYTEYWSGSNSGNQKWEAVQKI 418	299 MKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTT 358	243 SKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEE 298 ::::: : : :: : : : : : : : : : : :	188 VISKTFQLSSHEILGDWSIQVQVNDQTYYQSFQVSEYVLFKEEVTLQTPLYCSWN 242 182 FF-WPYNLPDLVSLGTWRIVAKYEHSPENYTAYFDVRKYVLPSFEVRLQPSEKFFYIDGN 240	RISVPYQTDKALYKPKQEVKERIVTLESDFKPYKTSLNILIKDPKSNILQQWL6QQSDLGFLFIQTDKGIYTPGSPVLXRVFSMDHNTSKMNKTVIVEFQTPEGILVSSNSVDLN	

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RESULT 9
US-08-447-411-45
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                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/043,747
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 1, 5
CITY: Arlington
CITY: Virginia
"1 S.A.
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APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
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                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
                                          TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEE 1533
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1755 S. Jefferson Davis Highway, Suite
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Best Local Similarity
                                                                                                                                                                   747
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    857 -- CSASTKGQRYRQQFPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEALWSDGVRKKLK
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                                                                                                                    LGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDI
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                                        LMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLG--EIPITVTALSPTASDAVTQMIL
                                                                                    I-CVAEPYEIRVMKVFFIDLQMPYSVVKNEQVEIRAILHNYVNEDIYVRVELLYNPAF--
                                                                                                                                                                 S-----RSDFPKSWLWLTKDLTEEPNSQGISSKTMSFYLRDSITTWVVLAVSFTPTKG
                                                                                                                                                                                                           SLGSSPHVRKHFPETWIWL-----DTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLG
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                                                                                                                                                                                                                                                      MGYTCEKRAKYIQEGDACKAAFLECCRYİKGVRDENQRESELFLARDDNEDGFİADSDII
                                                                                                                                                                                                                                                                                          -----YIDGVYD-NAEYAERFM--EENE-GHIVDIHDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTT
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PATENT NO. 5922320

GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PR
UMMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-662-227-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Apprix
Sequence 35, Apprix
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                               ADDRESSEE: OBLOW, GLANDERSSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                     COUNTRY: U
ZIP: 22202
      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYLGEVDSTMTIIDISMLTGFLFDAEDLTRLSKGVDRYISRYEVDNNMAQKVAVIIYLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFSGPGRSGMALMEVNILSGFMVPSEAIS-----LSETVKKVEYDHGKLN-----LYLDS 1336
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                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                     RECOMBINANT PROCVE
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Best Local Similarity
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                   NSWTPKACVIVYYIEDDGEIISDVLKIPVQ-----LVFK--NKIKLYWSKVKAEPSEKV
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IHDFSLGSSPHVRKHFPETWIWL-----DTNMGYRIYQEFEVTVPDSITSWVATGFVIS 728
                                        HENPMGYTCEKRAKYIQEGDACKAAFLECCRYIKGVRDENQRESELFLARDDNEDGFIAD
                                                                                                                     DAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAEFQDQDLRKCCEDVM
                                                                                                                                                             ECGLWVLTDANL-TKD-----
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                                                                             -YIDGVYD-NAEYAERFM--EENE-GHIVD
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RESULT 11
US-09-017-947-35
                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
STREET: 1/J
STREET: 1/J
CITY: ARLINGTON
                                                                                                                                                      APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVE
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 KKLKVVPEGVQKSIVTIVKLDPRAKGVGGTQLEVIKARKLDDRVPDTEIETKIIIQGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            847 QMILVKAEGIEKSYSQSILLDLTDNRLQST-----LKTLSFSFPPNTVTGSERVQITAI
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                                                                                                                                                                                                                                                             VOGEL, CARL-WILHELM
BREDEHORST, REINHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1648 amino aci-
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                        351 PKYFKPGMPYELTVYVTNPDGSPA-----AHVPVVSEAF-----HSMGTTLSDGTA 396
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                                                                 523 NSWTPKACVIVYYIEDDGEIISDVLKIPVQ-----LVFK--NKIKLYWSKVKAEPSEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 LGVISKTFQLSSHPILGDWSI---QVQVNDQTYYQSFQVSEYVLPKFEVTLQTP---LYCS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 RISVFIQTDXALYKPKQEVKFRIVTLFSDFKPYKTSLNILI--KDPKSNLIQQWLSQQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 QTRVDMNPAGGMLVT---PTIEIPAKEVSTDSRQNQYVVVQVTGPQVRLEKVVLLSYQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 NLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127
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                 LIPSPR--FVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGDNLIQMPGAAMKIKLEGDF
                                                                                                                                                                                                                                                                                                                                                                                                       DTFRSRFPNLNELVGHTLYAS-----VTVMTESGSDMVVTEQSGIHIVASPYQIHFTKT 350
                                                                                                                                                              IKVGS--PFELVVSGN----KRLKELSYMVVSRGQLVAVGKQNS----TM-FSLTPE
                                                                                                                                                                                                        KLILNIPLNAQ----SLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTE
                                                                                                                                                                                                                                                                                                                                                       TTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDY 356
                                                                                                                                                                                                                                                        KINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDEN
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                                                                                                              I KPGDNLPVNFNVKGNANSLKQI KYFTYLI LNKGKI FKVGRQPRRDGQNLVTMNLHI TPD
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RESULT 12
US-08-447-411-76
; Sequence 76, Application US/08447411
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KICTRYLGEVDSTWTIIDISMLTGFLPDAEDLTRLSKGVDRYISRYEVDNNMAQKVAVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCF-LEADFYIDIDQNVLHRTY 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDVLGPSING--LASLIRMPYGCGEQNMINFAPNI---YILDYLTKKKQLTDNLKEKALS
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                                                                                                                        IGNVCRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEPAX: 248855 OPAT UR
TOPORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 1333 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT IMPORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
PREPERMANCE: 07-CFFF NUMBER: 2126-101-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.5%; Score 768.5; DB 1; Best Local Similarity 24.4%; Pred. No. 9.7e-55; Matches 301; Conservative 208; Mismatches 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5773243
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FRIDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING
NUMBER OF SEQUENCES: 81
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COUNTRY:
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    -----KDYIDGVYDN------AEYAERFMEENEG-------
                                                                         AGSGQNNLGVFEDAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAQFQ 353
                                                                                                                                                                                                                                                                                                     M-FSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQ-----LVFK-----NKIKLY
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Y: U.S.A.
                                                                                                                   LGMFMNSFAVFQECGLWVLTDANLT-----
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                                                                                                                                                                                                             WSKVKAEPSEKVSLRISVTOPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYY
                                                                                                                                                                                                                                                          MNLHITPD--LIPSFRFVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGATSRDNRIQM-
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTLSDGTAKLFLNTPQNAQ---SLPITVRTNHGDLPRERQAIKSMTATAYQTQGGSGNYL
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RESULT 13
US-08-662-227-34
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                       APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, N
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORS
APPLICANT: KOCK, MICHAEL
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-----KENKDDLNHVDLNVCTSFSGPGRSGMALMEVNLLSGFMVPSEAIS-LSETVK 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LAVVQPMAVN----ISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVA 1269
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NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 34:
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Best Local Similarity
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LENGTH: 1333 amino acidi
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: US/08/62,227
FILING DATE: 14-UW-1996
CLASSIFICATION: 530
ATTROBUTO /ATTRIBUTO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING XYSTEM: PC-DOS/MS-DOS
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ADKDIYVRVELLYSPAFCSASTESQ----RYREQLPIKALSSRAVSFVIVPLEQGLHDVE 578
                                                      LKDATEVKVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLG--EIP
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CLASSIFICATION:

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RESULT 14
US-09-017-947-34
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APPLICANT:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RECOMBINANT PROCVE NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                           STREET: 1755 S.
CITY: ARLINGTON
FILING DATE:
                                                                                                                                                         COUNTRY: U
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1755 S.
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BREDEHORST, REINHORST
KOCK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                            FRITZINGER, DAVID
                                                                                                                                                                                                                                                                           OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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KKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCF-LEA 999
                                      DTEIETKITIQGDPVAQTIENSIDGSKLNHLIITPFGCGEQNMIRMTAPVIATYYLDTTQ 698
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                                                                             PNTVTGSERVQITAIGDVLGPSING--LASLIRMPYGCGEONMINF-APNI--YILDYLT
                                                                                                                      VTASVQGELMSDGVKKKLKVVPEGEWKSIVTIIELDPHTKGIGGTQVELVKANKLNDRVP
                                                                                                                                                             ITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQST-----LKTLSFSFP
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RESULT 15
US-07-779-172A-3
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Patent No. 5322838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Silberstein, David S.
APPLICANT: Minkoff, Marjorie
TITLE OF INVENTION: INHIB, A Factor Which Inhibits
TITLE OF INVENTION: Cytokine-Activated Leukocytes
NUMBER OF SEQUENCES: 3
TELEFAX: (202) 833-8716
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
                                                                                                                                                    CLASSIFICATION: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
NAME: Fox, Samuel L.
NAME: Fox, Samuel L.
                                                                                                REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19911016
                                                                                                                                                                                                                                                                                                                        ZIP: 20036-2678
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C
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WDVVEKADIGCTPGSGKDYAGVFSDAGL
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Search completed: January 15, 2004, 18:15:19 Job time: 33 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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       2 US-10-108-260A-3396

2 US-10-369-493-5314

2 US-10-369-493-5313

12 US-10-292-081A-15

14 US-10-922-081A-10

12 US-09-873-403-5

12 US-09-873-403-5

12 US-10-292-081A-12

12 US-10-292-081A-13

12 US-10-292-081A-13

12 US-10-292-081A-38

12 US-10-331-496A-38

12 US-09-756-247-2

12 US-09-756-247-2

12 US-09-756-247-2

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19 US-09-981-151A-10
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Sequence 3396, Ap
Sequence 5313, Appl
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Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
FIITE OF INVENTION: No. US20040005560A1el full length cDN
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3396

LENGTH: 665
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; Pred. No. 4.9e-268;
0; Mismatches 0;
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Scoring table: Sequence: Title: Perfect score:

Sequence 24, Appl Sequence 269, App Sequence 1394, App Sequence 126, Appl Sequence 35, Appl Sequence 36, Appl Sequence 36, Appl Sequence 37, Appl Sequence 42, Appl Sequence 42, Appl Sequence 22, Appl Sequence 22, Appl Sequence 59, Appl Sequence 6, Appl Sequence 6, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 139, App Sequence 139

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Regult

Score

Query

Length DB

665; 0,

Gaps

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APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 5314

LENGTH: 1508

TYPE: PAT

ORGANISM: Caenorhabditis elegans

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Best Local (
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                                     TFQLSSHPILGDWSIQVQ----VNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMNSKHLN 247
                                                                                                                                         VISNL-KPGIAQTYSLSEMPAQSLTPRQSYKLYIRGETLNAELIFENENELKYDQKALSV
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                ELQLAEETLIGDWFIEVETSNGVQDKS---SFTVDTYVLPKFEVNIKTSSFITIND-DLS
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                                                                                                                                                                                                                                                                                                                                                 SAQKKVEKLKESRAYMFQARPVDIETTSYAVLSYLAQNQTSESLSIIRWLVSQRNELGGF
                                                                                                               VSSE--SKLSDS----WQPRSLDIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGF
                                                                                                                                                                                       DVQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKEALNMLTWR--AEQEGGMQFW 1124
                                                                                                                                                                                                                                                                                    QLETKAIKFIEQGIQRELTYKRADNSFSAFGDSDKAGSTWLTAFVVRSFHHAKQYAFVDP
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 AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNV
                                TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
                                                            ASTODTTVALKALSEFAALMNTERTNIQVTV-TGPSSPS-----PLAVVQPM-----
                                                                                                                                                         ENGKAVTYLEKHLDEVSGNAYTMAVVAYALQLAKSKQAGKAFENLKKHKI VEKSGDVKFA
                                                                                                                                                                                                                        NVISRAVAFLNSQQMESGAFAERGEVHHKDMQGGAQDGGVALTAFVLISIL-----ENGM
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5313
LENGTH: 1519
TYPE: PRT
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Matches 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 25.2%; Score 1850; DB 12; Local Similarity 31.6%; Pred. No. 9.9e-143; tes 477; Conservative 290; Mismatches 563;
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                                                                                                                                    IIEFFDYTTVLKPSLNFTATVKVTRADGN--QLTLEERRNNVVITVTQRNYTEYWSGSNS
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                                                                                                                                                                                                                                                                                                                                                         TFQLSSHPILGDWSIQVQ----VNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMNSKHLN
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                                    SLOBEKETKIVEVDAHGTSVLTLOPPINCTSARIEAH-YDIGGKDNFTATPIYSSLYVEA
                                                                     GNOMEAVOKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-----
                                                                                                                                                                                AAVVFSNDELKR------HKLLHEWGGGSIRIVASVTEDITEIERNATHQISTFREEV
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                                                                                                         KLDVEKQGDTFKPGLTYNVVVALKQMDDTPVKATLPKR----VQVSTFYNYP--YNHDTS
--SPSKTYIQLKTRDEN-IKVGSPFELVVSGNKRLKELSYMVVSRGQLV-----AVGKQN
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                                                     KCG--EDCWP 1483
                                                                                        LCSDVQGCRP 1398
                                                                                                                            KMNVYFNPLGGRPVCLSLYSDVTYQVADQKPANFRLVDYYDPEEQLKMTYAAKQTRSLQE 1475
                                                                                                                                                             KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.6%; Score 1441; DB 12; Best Local Similarity 29.2%; Pred. No. 5.5e-109; Matches 453; Conservative 264; Mismatches 551;
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/292,081A CURRENT FILING DATE: 2002-11-08 PRIOR APPLICATION NUMBER: 60/337434 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 15 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kenneth David Becker APPLICANT: Gonul Velicelebi APPLICANT: Xin Wang APPLICANT: Randolph B. Tanzi APPLICANT: Lars Bertram APPLICANT: Aleister J. Saunders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGIC
FILE REFERENCE: 37481-3323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                      EIISDVLKIPVQLVFKVKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLM- 599
                                                                                                               LKELS--YMVVSRGQLVAVG-----KQNST----MFSLTPENSWTPKACVIVYYIEDDG
                                                                                                                                                                                                                                                                                                                  VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
                                                                                                                                                                                                                                                                                                                                                                        EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
                                                                                                                                                                                                                              TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP-----ILEDS
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                           DVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAA-PQSVCALRAVDQSVLLMK 608
                                                                                                                                           EEAHHTAY--
                                                                                                                                                                      SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS----PFELVVSGNK--R
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                                                                                   LKKLSFYYLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPVKSDIAPVARLLIYAVLPTG 549
                                                                                                                                                                                                  FI-RGNEANYY--SNATTDEHGLVQFSINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEH
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No. US20030162202A1
                                                                                                                                          ----LVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTLLG 489
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Pred. No. 5.5e-109;
 -NDITMENVVHELELYNTGY-YLGMFMNS----FA 631
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                                                                                                                             EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
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                                                           KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS
                                                                                                                                                                                              DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG
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US-10-052-817-2

Sequence 2, Application US/10052817

Publication No. US20020114792A1

; GENERAL INFORMATION:

APPLICANT: Tanzi, Rudolph E.

APPLICANT: Kovaces, Dora

; APPLICANT: Saunders, Aleister J.

; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies

; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies

; TITLE OF INVENTION: Alpha-10-Macroglobulin Therapies

; CURRENT APPLICATION UNMER: US/10/052,817

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Screening Methods for

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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 1474
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/093,297
PRIOR FILING DATE: 1998-07-17
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FILING DATE: 1999-02-02
APPLICATION NUMBER: 09/148,503
FILING DATE: 1998-09-04
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PHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDTITEWKAGAFCLSEDAGIGISS
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; TYPE: PRT
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                                                                               CURRENT APPLICATION NUMBER: US/09/873,403
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/625,139
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/209,266
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 5, Application US/09873403
Patent No. US20020028207A1
GENERAL INFORMATION:
APPLICANT: Srivstava, Pramod K
TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY
FILE REFERENCE: 8449-178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                      PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVS---EELSLKLPPNVVEESARAS
                                                                                                                                                                                                                                                                                   GSSPH----VRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTT 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP-----ILEDS 438
                                                                     ----SDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQ 896
                                                                                                                                                                                                                TPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSS
                                                                                                                                                                                                                                                                                                                                                                                                                           ASNDITMENVVHEL-ELYNTGY------YLGMFMNS------FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAA-PQSVCALRAVDQSVLLMK 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHLNGTITAKYTYGKPVKGDVTLTFLPL-------SFWGK 276
                                                                                                                                          E----INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS------PTA 841
                                                                                                                                                                                                                                                                                                                      FLEDMGLKAFTNSKIRKPKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHVEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMN 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEAHHTAY------LVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTLLG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGISRNVSTNVFFKOHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGVISKTFQLSSHPILGDWSIQVQVND--QTYYQSFQVSEYVLPKFEVTLQTPLYCSMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDSLVFVQTDKSIYKFGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTDLEAENDVLHCVAF----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN
 ITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSF 956
                                                                                                           EQAPHCICANGRQ-----TVSWAVTPKSLGNVNFTVSAEALESQELCGTEVPSV 890
                                                                                                                                                                             T-ASLRAFOPFFVELTMPYSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPVEK 841
                                                                                                                                                                                                                                                                                                                                                           VFQECGLWVLTDANLTKDYIDGVYDNAE-----YAERFMEENEGHIVDIHDFSL
                                                                                                                                                                                                                                                                                                                                                                                          PDAELSASSVYNLLPEKDLTGFFGFLNDQDDEDCINRHNVYINGITYTPVSSTNEKDMYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKELS--YMVVSRGQLVAVG-----KONST----MFSLTPENSWTPKACVIVYYIEDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS----PFELVVSGNK--R 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FI-RGNEANYY--SNATTDEHGLVOFSINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEH 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT-----TVTESV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
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                                                                                                                                                                                                                                                  PHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDTITEWKAGAFCLSEDAGLGISS
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RESULT 7 US-10-292-081A-10

Sequence 10, Application US/10292081A Publication No. US20030162202A1

GENERAL INFORMATION:

APPLICANT: Kenneth David Becker APPLICANT: Gonul Velicelebi

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1414 HVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNA 1465
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                                                                                                                                                                                                                                                                                                OKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKOONAQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWLSQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFC
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                                                                                                             DLN-HVDLNVCTSFSGPG---RSGMALMEVNILLSGFMVPSEAISL---SETVKKVEYDHG 1328
                                                                                                                                                    LPELPGEYSMKVTGEGCVYLQTSLKYNI------LPEKEEFPFALGVQTLPQTCD
                                                                                                                                                                                                                                                   GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ------------
                                                                                                                                                                                                                                                                                                                      TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF 1074
                                     KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS
                                                                          EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
                                                                                                                                                                                     ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
                                                                                                                                                                                                                            GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
                                                                                                                                                                                                                                                                                                                                                                            LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP 1186
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                                     1380
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TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLOU
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR PELICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1474
                                                                                                             Query Match
Best Local Similarity
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-10-292-081A-10
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                                                                                            19.6%; Score 1440; DB 12; al Similarity 29.1%; Pred. No. 6.7e-109; 451; Conservative 266; Mismatches 551;
                                              12 LLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTV
  LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
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                                                                                              Indels
                                                                                                                                       Length 1474;
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72 -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET

FTDLEAENDVLHCVAF-----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN

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                                                                                                                                                                                                                                           MRQGYQRELLYQREDGSFSAFG-NYDPS-GSTWLSAFVLRCFLEADPYIDIDQNVLHRTY
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                                                                   IWLSQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFC
                                                                                                                                    TWLKGHOKSNGEFWDPGRVIHSELQGGNKSPVTLTAXIVTSLLGYRKYQPNIDVQESIHF
                                                                                                                                                                                                           LNTGYQRQLNYKHYDGSYSTFGERYGRNQGNTWLTAFVLKTFAQARAYIFIDEAHITQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVS---EELSLKLPPNVVEESARAS
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                                                                                                244 KHLNGTITAKYTYGKPVKGDVTLTFLPL----
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                            EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ 303
                                                                                                                                                                                                                                                                                                            EDSLVFVQTDKSIYKPGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFQLE
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                                                                                                                                                                    GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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HVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNA 1465
                                                                                                                                                          EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
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                                                                                                                                                                                                                                 DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG
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APPLICANT: Kenneth David Becker
APPLICANT: Gonul Velicelebi
APPLICANT: AIN Wang
APPLICANT: Randolph E. Tanzi
APPLICANT: Lars Bertram
APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE PO
FILE REFERENCE: 37481-3323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10292081A Publication No. US20030162202A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/292,081A CURRENT FILING DATE: 2002-11-08 PRIOR APPLICATION NUMBER: 60/337434 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 15
12 LLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTV 71
                                                    19.6%; Score 1440; DB 12; 29.1%; Pred. No. 6.7e-109; vative 266; Mismatches 551;
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                                                       Indels 284;
                                                                                                           Length 1474;
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                                                                                                                                 GGFASTQDTTVALKALSEFAALMVTERTNIQVTVTGPSSPSPLAVVQ-----
                                                                                                                                                                                                  QKPKAPVGHFYEPQAPSAEVENTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1245
                                                                                                                                                                                                                                                                   VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
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----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD 1275
                                                                    GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
                                                                                                                                                                                                                                                                                                                                       LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP 1186
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PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/10292081A Publication No. US20030162202A1
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TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 37481-3323
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FI-RGNEANYY--SNATTDEHGLVQFSINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEH
                                TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP-----ILEDS 438
                                                                                                                                           VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
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                                                                                                       TGISRNVSTNVFFKOHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNOLTLEERRNNVVI
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                                                                                                                                                                                                                  EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
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     HVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNA 1465
                                                 KLNLYLDSYNETQFCVNIPAVRNFKYSNTQDASYSIVDYYEPRRQAVRSYNS 1380
                                                                                                                                                                                                                  LPELPGEYSMKVTGEGCVYLQTSLKYNI------LPEKEEFPFALGVQTLPQTCD
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US-10-331-496A-38
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US-10-331-496A-38
; Sequence 38, Application US/10331496A
; Publication No. US20030228305A1
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PRIOR APPLICATION NUMBER: US 60/366,284
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR APPLICATION NUMBER: US 60/405,645
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PRIOR FILLING DATE: 2002-01-02
PRIOR PELLICATION NUMBER: US 60/351,885
PRIOR FILLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR PELLING DATE: 2002-02-25
PRIOR PELLICATION NUMBER: US 60/362,004
PRIOR FILLING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR APPLICATION NUMBER: US 60/366,869
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SEQ ID NO 38
LENGTH: 1474
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CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
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VK--TKVFQLKR-----KEYEMK-----LHTEAQIQEEGTVVELTGRQSSEITRTI
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                                                                                                                                                                                                                                                                                                                                                    KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT----TVTESV 331
                                                                                                         EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
                                                                                                                                                                                                                  GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
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DLN-HVDLNVCTSFSGPG----RSGMALMEVNLLSGFMVFSEAISL---SETVKKVEYDHG
                                                                              LPELPGEYSMKVTGEGCVYLQTSLKYNI
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                                                                                                                                                                                     GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1304
                                                                                                                                                                                                                                                                                                                                            VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
                                                                                                                                                                                                                                                                                                                                                                                               LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP 1186
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                                                                                                                               PMAVNISANGEGEAICQLNVVYNVKASGSSRRRRSIQNQEAEDLDVAVK---ENKD
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APPLICANT: L1U, CHENGLING
APPLICANT: Yeung, George
APPLICANT: Yeung, George
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS REL
TITLE OF INVENTION: METHODS AND MATERIALS REL
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-31CIP
CURRENT APPLICATION NUMBER: U9/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR RILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/644,711
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/664,711
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR PILING DATE: 09/560,875
PRIOR PILING DATE: 09/496,914
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1508
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030180722A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
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TDKTGCFSAPVDMATFDLIGYAYSHQINIVATVVEEGTGVEANATQNIYISPQMGSMTFE
                                                                                                                                                    QTDKPLYTPGQQVYFRIVTMDSNFVFVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLS
                                                                                                                                                                                                                                                                   QTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQWLSQQSDLGVISKT 192
                                                                                                                                                                                                                                                                                                            RYTYGKPMLGAVQVSVC-----QKAN-----TYWYREVEREQLPDKCRNLSGQ 285
                                                                                                                KYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEY
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                                       LD----LSSP-----
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Tang, Y. Tom
Liu, Chenghua
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Mize, Nancy K
Deng, Cenhua
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Arterburn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%; Score 1437.5; DB 12; Length 1508; ilarity 27.1%; Pred. No. 1.1e-108; Conservative 274; Mismatches 552; Indels 307; Gaps
                                   --GPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFF
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34	-GPSSPSPLAVVQPMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEA
1210 1295	1159 SEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVT :: : : :
1158 1235	1107 ALNMLTWRAEQEGGMQFWVSSESKLSDSW-QPRSLDIEVAAYALLSHFLQFQT
1106 1175	1048 LTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKB- : : : : : : : 1117 LTAYVTAALLEMGKDVDDPNVSQGLRCLKNS-ATSTTNLYTQALLAYIFSLAGEMDIRNI
1047 1116	988 LSAFVLRCFLBADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDDGRVIHSELQGGNKSPVT : : : : : :
987 1056	928 NFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTW - - - - - - - - - - -
927 996	889 VTGSERVQITAIG
888 936	838SPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLGPSFPPNT : : : : : : : : : : : : : : : : :
83 <i>7</i> 881	787 SDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTAL
786 827	727 ISEDIGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEK -
726 768	667 ENEGHIVDIHDFSLGSSPHVRKHFPETWIWLDTNMGVRIYQEFEVTVPDSITSWVATGFV :-
666 716	627ERFAVEQECGLWVLTDANLTKDYIDGVYDNAEYAERFWE
626 657	608 ENVVHELELYNTGYYLGMF
607	548 KIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLANASNDITM
547 550	498 YMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVL ::: ::: : : :: : 191 YYLIGKGSLVMEGQKHLNSKKKGLKASFSLSLTFTSRLAPDPSLVIYAIFPSGGVVADKI
497 490	447 FLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELS : ::
446 445	398YTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAY ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
397 400	355 DYTTVLKPSLNFTATVKVTRADGNOLTLEERRNNVVITVTQRN

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CURRENT APPLICATION NUMBER: US/09/756,247
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PRILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/644,711
PRIOR APPLICATION NUMBER: 09/664,711
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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PRIOR APPLICATION NUMBER:
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO ALPHA-2-MACROGLOBULIN-LIKE
TITLE OF INVENTION: AND POLYNUCLEOTIDES
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Local Similarity 29.0%; Pred. No. 2.5e-108;
Les 450; Conservative 265; Mismatches 551;
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                                                                                                                                                                                                                                                                        186 LGVISKTFQLSSHPILGDWSIQVQVND--QTYYQSFQVSEYVLPKFEVTLQTPLYCSMNS
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277 KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT----TVTESV 331
                                                                                                                                                    244 KHLNGTITAKYTYGKPVKGDVTLTFLPL-----
                                                                                                                                                                                                                                                                                                                                                                                    112 EDSLVFVQTDKSIYKPGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FTDLEAENDVLHCVAF-----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET 126
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Deng, Cenhua
Goodrich, Ryle
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                                                                        EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
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Tang, Y. Tom
Liu, Chenghua
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                                                                                                                                                                                                                               VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
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LNTGYQRQLNYKHYDGSYSTFGERYGRNQGNTWLTAFVLKTFAQARAYIFIDEAHITQAL 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS----PFELVVSGNK--R 492
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----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD 1275
                                                                                                                                        GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ-------
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                                                                                 GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1291
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; SEQ ID NO 25
; LENGTH: 1491
; TYPE: PRT
; ORGANISM: hono sapiens
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APPLICANT: Liu, Chenghua
APPLICANT: Yeung, George
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APPLICANT: Yeung, George
APPLICANT: D'IMAIRE, RADOJE T
TITLE OF INVENTION: METHODS AND MATERIALS REI
TITLE OF INVENTION: AND POLYMUCLEOTIDES
FILE REFERENCE: HYS-31CIP
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/640,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/684,711
PRIOR APPLICATION NUMBER: 09/660,875
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-04-27
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                                                                                    YT--VAVAEGKTFGTFSVEEYVLPKFKVEVVEPKELSTVQESFLVKICCRYTYGKPMLGA
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VQVSVC-----QKAN------TYWYREVEREQLPDKCRNLSGQTDKTGCFSAPV
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Mize, Nancy K
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                                                                                               RQRNSLGGFASTQDTTVALKALSEFA--ALMNTERTNIQVTVT------GPSSPSPLAV 1220
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Sequence 9, Application US/10292081A

Publication No. US20030162202A1

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APPLICANT: Lars Bertram

APPLICANT: Aleister J. Saunders

TITLE OF INVENTION SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLO

FILE REFERENCE: 37481-3323

CURRENT APPLICATION NUMBER: US/10/292,081A

CURRENT APPLICATION NUMBER: 60/337434

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PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 15

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FI-RGNEANYY--SNATTDEHGLVQFSINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEH
                                TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP------ILEDS 438
                                                                                                                                                    VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
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                                                                           TKLS-FVKVDSHFRQG---IPFFG----
                                                                                                                TGISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI 391
                                                                                                                                                                                                                                EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
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                                                                           -QVRLVDGKGVPIP----NKVI
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LCS-----DVQGCRPCEDGASGSHHHSSVIFIF 1416

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HVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYE-----TGDLQLLSTM 1464
                                                                                                                                                                                                                                   LPELPGEYSMKVTGEGCVYLQTSLKXNI-----LPEKEEFPFALGVQTLPQTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1245
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                                                    KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCD 1386
                                                                                                              EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSPH----VRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTT 737
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                                                                                                                                                                      DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG
                                                                                                                                                                                                                                                                                           ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IWLSQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFC 1127
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US-09-981-151A-10
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PRIOR FILING DATE: 2000-10-17
PRIOR PELICATION NUMBER: 60/241,243
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,611
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,612
PRIOR PILING DATE: 2000-10-23
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PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,880
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,880
                                                                                                                                                                                                                                       SOFTWARE: PA
SEQ ID NO 10
LENGTH: 149
                                                                                                         Query Match
Best Local :
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APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
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                                                                                    Matches
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CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/242,881 PRIOR FILING DATE: 2000-10-24
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                                    20 LAVAPG-----PRFLVTAPGIIR-PGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSV
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Spytek, Kimberly A
Spytek, Kimberly A
Gangolli, Esha A
LALSPAIAEELPNYLVTLPARLNFP----SVQKVCLDLSPGYSDVKFTVTLETKDKTQKL
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Peyman, John A
Stone, David J
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Taupier Jr, Raymond i
Burgess, Catherine E
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Malyankar, Muriel M
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                                                                                       Conservative
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                                                                                  19.3%; Score 1421.5; DB 12; 27.2%; Pred. No. 2.3e-107; tive 269; Mismatches 559; I
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824 RŸQTDLAKSH 838 878 LDSNEPCGGG 883 SFPPNTVTGS 936 ELPVDIVPGS 943 KQLTUNLKEN 996 GLLTEEIRSH 1003 IDIDQNVLHH		51 90 00 00 00 00 00 00 00 00 00 00 00 00	74 LEABGVFEKG
RVQTDLAKŚHEYQLESWADSQTSSCLCADDAKTHIWNITAVKLĞHİNFİISTKISPTASDAVTQMILVKABGIEKSYSQSILLDLTDNRLQSTLKTLSF	SE LI LI LI SE L	SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVS : ::	ADEI : :
SSCICADDAKTHHWNITA VKABGIEKSYSQSIILLDI :	-MNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEYA	SSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVV : :	YELRVTGRTQDEILESNS
VKLGHİNPTİSTKI 877 ITDNRLQSTLKTLSF 882 KGGKVAS - ESVSL 935 FAPNIYILDYLTKK 942			TGRTQDEILFSNSTRLSFETKRISVFI 133 :

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123PMAVNISANGFGFAICQLNVYNVKASGSSRRRRSIQNQEAFDLDVAVKENK 1274 1295 LDNVPGMYTLEASGQGCVYVQTVLRYNILPPTNNKTFSLSVEIGKARCEQP 1345 1275 DDLNHVDLNVCTSFSGP-GRSGMALMEVNLLSGFMVPSEAISLSE-TVKKVEYDHGKL 1330 1276 TSPRSLTLTIHTSYVGSRSSSNMAIVEVKMLSGFSPMEGTNQLLLQQPLVKKVEFGTDTL 1405 1331 NLYLDSVNETQFCVNIPAVRNEKVSNTQDASVSTVDYYEP 1370 1406 NIYLDELIKNTQTYTFTISQSVLVTNLKPATIKVYDYYLP 1445	1063 QPNIDVQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKE-ALNMLTWRABQBGGM 1121	: : : : : : : :

Search completed: January 15, 2004, 18:19:33 Job time: 51 secs

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us-10-020-095-3.rni

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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4287
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Gapop 10.0 , Gapext 1.0
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Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	U	4.	ω	2	سر	ult No.
37	37	37.2	37.2	37.2	37.2	37.2	37.4	37.8	37.8	38	38.2	38.6	38.6	38.8	38.8	39.4	40	41.4	41.4	44	44	46.4	47.2	47.4	110	110	Score
0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0	1.0	1.0	1.0	1.1	1.1	1.1	2.6	2.6	Query Match Length
1311	987	53500	1707	526	526	526	1152	28171	1062	30549	3027	1680	1579	3981	1327	15016	1581	1664976	5398	750	333	5211	339	7218	4577	4079	
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US-09-252-991A-10198	US-09-252-991A-9774	US-09-266-965-76	US-09-266-965-68	US-09-265-503B-14	US-08-352-902D-14	US-08-961-810-14	US-09-107-532A-2119	US-08-961-527-22	US-09-134-001C-1803	US-09-134-001C-322	US-09-328-352-3277	US-09-071-035-81	US-09-071-035-83	US-08-955-138-2	US-09-350-756-9	US-09-601-198-60	US-09-601-198-80	US-08-916-421B-1	US-09-356-952-11	US-09-241-606-3	US-09-241-606-5	US-08-447-411-1	US-09-311-352B-1	US-08-232-463-14	US-09-241-606-1	US-09-016-434-1174	ID
10198,	9774	76,	68	14,	14,	Sequence 14, Appl	211	Sequence 22, Appl	180	322, F	327	81,	83,	2	9,	60,	õ	e 1,	11,	ω	Sequence 5, Appli	1,	1, A	14,	Sequence 1, Appli	Sequence 1174, Ap	Description

C 29 37 0.9 2274 4 US-09-620-312D-154 30 37 0.9 4248 4 US-09-522-991A-9867 31 36.4 0.8 1956 4 US-08-662-227-1 32 36.4 0.8 5948 2 US-08-662-227-1 34 36.4 0.8 5948 2 US-08-662-227-1 35 36 0.8 5948 2 US-08-662-227-1 36 37 35.8 0.8 5827 4 US-09-813-133A-3 37 35.8 0.8 426 4 US-09-813-133A-3 38 35.8 0.8 426 4 US-09-813-132B-3 39 35.8 0.8 2478 4 US-09-811-198-41 37 35.8 0.8 8855 2 US-08-322-760A-1 38 35.8 0.8 8855 2 US-08-322-760A-1 39 35.8 0.8 8855 2 US-08-326-949-1 42 35.4 0.8 1029 3 US-09-077-675A-4 43 35.4 0.8 1167 4 US-09-073-674-4 43 35.4 0.8 1167 4 US-09-038-003-6 45 35.4 0.8 1167 4 US-09-220-132-94
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US-09-23-91A-9867 US-09-252-991A-9867 US-08-259-8968-1 US-08-257-1 US-08-662-227-1 US-08-662-227-1 US-09-601-198-41 US-09-601-198-41 US-09-601-198-52 US-09-601-198-52 US-09-601-198-52 US-09-601-198-52 US-09-601-198-52 US-09-601-198-52 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54 US-09-601-198-54

ALIGNMENTS

RESULT 1 US-09-016-434-1174

Sequence 1174, Application US/09016434 Patent No. 6500938

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; LIBRARY: GENBA;
; CLONE: g177869
US-09-016-434-1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERBWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
Query Match
Best Local Similarity
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APPLICANT: Jeffrey J. Sellhamer
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                     TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                        LENGTH: 4079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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3174 PORTER DRIVE
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2.6%;
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Pred. No. 3.1e-21;
                  Length 4079;
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Gaps

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APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-241-606-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09241606 Patent No. 6472140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (44)..(112)
                          NAME/KEY: CDS
LOCATION: (44)..(4468)
        FEATURE:
                                                                                                                                                                                              ENGTH: 4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303;
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| Sequence 14, Application US/08232463 |
| Patent No. 5670367 |
| GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHENGER, F. APPLICANT: FALXMER, F. G. |
| APPLICANT: FALXMER, F. G. |
| APPLICANT: FALXMER, F. G. |
| NUMBER OF SEQUENCES: 52
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; LOCATION: (113)..(4468)
US-09-241-606-1
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Best Local Similarity 50.2%;
Matches 303; Conservative
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                  STREET: 1800 Dia
CITY: Alexandria
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Pred. No. 3.3e-21;
0; Mismatches 295;
                                                                                                                                                          Suite
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                                                                                                                                         RESULT 4
US-09-311-352B-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harr
                                                                                                          Sequence 1, Application US/09311352B Patent No. 6329500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conser
                                                                                             GENERAL INFORMATION:
APPLICANT: Webb, Donna J.
APPLICANT: Gonias, Steven L.
TITLE OF INVENTION: Transforming Growth Factor-beta Binding
FILE REFERENCE: 00370-02
CURRENT APPLICATION NUMBER: US/09/311,352B
CURRENT FILING DATE: 1999-05-13
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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APPLICATION NUMBER: U
FILING DATE:
APPLICATION NUMBER: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                  1509 GGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTC 1551
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                                                                                                                                                                                                                                                                  TGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTAGTATCCAG 1508
                                                                                                                                                                                                                                                                                                                          TAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGATCGCCTTT 1448
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In Release #1.0, Version #1.25
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RESULT 5
US-08-447-411-1
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                                                                                                                    APPLICATION
FILING DATE: 07-AFK-1332
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REGISTRATION UMBER: 1126-10
TELECOMMUNICATION INFORMATION:
TOLECOMMUNICATION 1413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                   TELEPHONE: (703) 413-30
TELEPAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: A
                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2176
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    Application US/08447411
    5773243

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arlington
                I: 5211 base pairs
nucleic acid
DEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACCATTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGAGGTGAAGAATT 2291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRITZINGER, DAVID C.
BREDEHORST, REINHARD
VOGEL, CARL-WILHELM
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unknown
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RESULT 7
US-09-241-606-3
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US-09-241-606-5
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LOCATION: (1)..(333)
OTHER INFORMATION: A
US-09-241-606-5
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                                                 Sequence 3, Application US/09241606
Patent No. 6472140
GENERAL INFORMATION:
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Best Local Similarity
Matches 113; Conserva
                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
               APPLICANT: Tanzi, Rudolph E. APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION:
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                                                                                                                                                                                    ACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCC 126
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Pred. No. 0.012;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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US-09-356-952-11
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TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 750
                                                                                                                                                                                                                                                                                                                   Query Match 1.0%;
Best Local Similarity 47.2%;
Matches 126; Conservative
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Best Local Similarity
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APPLICANT: Kuriyan, John
ITITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
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ORGANISM: Homo :
FEATURE:
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OTHER INFORMATION: A /LRP Binding Domain
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                                                             2791 CAAATTTTTGAAAAATTAAATAATGCTACAGGTGAACACTTAAAAATTATAAGTAAACCC 2850
                                                                                                                                                2731 AGGAAGAAAAATATCCATTAACTGTAGACACTTTGAATACAATGAAGAAGAAGAAATCCTCG 2790
982 ACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACTAATGTGTTCTTCAAGCAACAT
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                                                                                                                                                                                  GGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAAAATGTAATGGATTCTTCAAAT 921
                                                                                                  GGACTITCTGAATACCTGGATCTATCTTCCCCCTGGACCAGTAGAAATTTTAACCACAGTG 981
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Pred. No. 0.37;
0; Mismatches 141;
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Pred. No. 0.016;
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TITLE OF INVENTION:
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APPLICANT: Bult et
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Sequence 1, Application US/08916421B
Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Methar FEATURE: NAME/KEY: misc_1
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                                                                                                                            NAME/KEY: misc feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                              LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals
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LOCATION: (98343)
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OTHER INFORMATION: n equals
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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                             LOCATION: (191989) . (191989)
OTHER INFORMATION: n equals
                                                              LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
                                                                                                 COCATION: (148948)..(
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OTHER INFORMATION: n equals
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                     NAME/KEY:
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                                                                                                                     NAME/KEY: misc_feature
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NAME/KEY: misc feature LOCATION: (682442)...(682442) OTHER INFORMATION: n equals a, t NAME/KEY: misc feature LOCATION: (713652)...(713652) OTHER INFORMATION: n equals a, t NAME/KEY: misc_feature LOCATION: (741684) . (741684) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (779455) . (779455) LOCATION: (559241)...(559241)
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NAME/KEY: misc_feature NAME/KBY: misc_feature LOCATION: (871619).. (871619) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (1084830).. (108483 NAME/KEY: misc feature LOCATION: (674435)...(674435) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (231980)..(2) LOCATION: (855539)..(855539) OTHER INFORMATION: n equals NAME/KEY: misc LOCATION: (8555 NAME/KEY: misc_feature LOCATION: (779676)..(779676) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (657203)..(657203) NAME/KEY: misc feature LOCATION: (657081)..(657081) OTHER INFORMATION: n equals LOCATION: (600992)..(600992)
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LOCATION: (622708)..(622708) NAME/KEY: misc_feature LOCATION: (559241)..(55 OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (559167)...(559167) NAME/KEY: misc_feature LOCATION: (319226)..(319226) NAME/KEY: misc_feature LOCATION: (312993)..(312993) OTHER INFORMATION: n equals a, LOCATION: (309418)..(309418)
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APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT APPLICATION NUMBER: US/09/601,198
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                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local
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LOCATION: (1602912)..(1602912)
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; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-80
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APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
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Best Local Similarity 43.8%;
Matches 175; Conservative
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Query Match 0.9
Best Local Similarity 48.3
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                                                                                     ORGANISM: Ureaplasma urealyticum -09-601-198-60
                                                                                                                                                                                                                                                                        APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALIYICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
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PRIOR FILING DATE: 1998-01-30
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PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAGCCAATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTTGCTATTTTGTCAGCTCA 372
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                     0.9%;
    Score 39.4; DB Pred. No. 2.9; 0; Mismatches
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Pred. No. 0.4;
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                                          DB 4;
                                             Length 15016;
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US-09-350-756-9
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US-09-350-756-9
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                                                                                                                US-08-955-138-2/c
                                                                                                                                    RESULT 13
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LENGTH: 1327
TYPE: DNA
ORGANISM: Clostridium botulinum
                                                    Sequence 2, Application US/08955138A Patent No. 5977435
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09350756 Patent No. 6495143
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Best Local (
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TITLE OF INVENTION: Botulinum Neurotoxin Vaccine
FILE REFERENCE: 003/124/SAP RIID 98-21
CURRENT APPLICATION NUMBER: US/09/350,756
CURRENT FILING DATE: 1999-07-09
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Gellatly, Kevin S.
TITLE OF INVENTION: PLANT PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: US 60/092,416
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Michael D. Parker APPLICANT: Jonathan F. Smith APPLICANT: Mark T. Dertzbaugh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: U.S. Army Medical Reseach Institute for Infectious APPLICANT: John S. Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                            TTAATGTAGTAGTTAAAAATAA 1002
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Pred. No. 0.79;
0; Mismatches 102;
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; Sequence 83, Application; Patent No. 6448043; GENERAL INFORMATION; APPLICANT: Gill.
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US-09-071-035-83
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SEQ ID NO 2
LENGTH: 3981
TYPE: DNA
ORGANISM: SOLANUM TUBEROSUM
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Best Local Similarity 50.0%;
Matches 97; Conservative
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CURRENT FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 119
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                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                        COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1579 base pairs
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKST NUMBER:
                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                             TELEPHONE: (301)
                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences,
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o. 6448043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gil H. Choi
                                                                                                                                      (301)
                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 1.4Mb
                                                                                                                    309-8512
                                                                                                                                      309-8504
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Pred. No. 1.7;
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US-09-071-035-81
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                                                                                                                         Query Match 0.9%; Score 38.6; DB 4; Length 1680; Best Local Similarity 49.3%; Pred. No. 1.1; Matches 101; Conservative 0; Mismatches 104; Indels 0
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Best Local Similarity 49.3%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS:
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APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
REGISTRATION NUMBER: 95,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: HP Vectra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: ya. STREET: PARTY: Rockville CITY: Rockville Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       LENGTH: 1680 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                               1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 1680
  1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 CTATATTGGAGTAAAGTGAAAGCTG 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAATTCAACAATGTTCTCTTTAACA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 CAAAATGGTGCAGAAATCTCAGCGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AAAAAATGATTGATCCTAAAAACGGCTTTGTTTATAGCTTCCTCATCGTTGAAACAATT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 AAAGAAGCGGTTTGGAGTAACGATGATCCTGTCACAGCACATGATTTTGAATATGCTTGG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 GTAGCAAAAGCATTGCCGATGATTTCAGAAGATGGAAAAAACCTACACGATTTCTTTGAGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20850
                                            GTAGCAAAAGCATTGCCGATGATTTCAGAAGATGGAAAAACCTACACGATTTCTTTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09071035
                                                                                                                                                                                                                                                                                               1680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP Vectra 486/33
                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSDOS version 6.2
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Pred. No. 1;
0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 PB369P2
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                a a
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      2584.6
730.8
541.6
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272
272
194.4
1194.4
1136.8
130
136.8
126.8
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1126.8
1126.8
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                              Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2324096 seqs, 1762381658 residues
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                    US-09-833-381-1810
US-10-113-013-233
US-10-160-162-48
US-10-160-162-48
US-09-860-352-12867
US-10-027-632-204326
US-10-027-632-204326
US-10-316-253-266
US-10-316-253-268
US-10-316-253-268
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Compugen Ltd
Sequence 1810, Ap
Sequence 953, App
Sequence 223, App
Sequence 48, Appl
Sequence 48, Appl
Sequence 12867, Appl
Sequence 204326,
Sequence 266, App
Sequence 268, App
Sequence 3727, Ap
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 125, App
Sequence 125, App
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45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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13	11	12	13	13	13	13	13	15	14	13	13	13	13	12	10	9	13	13	9	9	13	13	13	ü	12	9	10	11	11
US-10-006-285-206	US-09-918-995-12615	US-10-094-886-123	US-09-756-247-27	US-09-971-429B-2	US-10-006-285-404	71-392-1	US-10-240-965-178	US-10-076-816-56	US-10-052-817-1	0-292	US-10-292-081A-3	US-09-960-706-654	9-873	US-10-331-496A-19	US-09-880-107-2236	US-09-873-403-3	US-10-292-081A-7	US-10-292-081A-2	US-09-873-403-4	US-09-925-301-552	-10-08	US-10-292-081A-4		US-09-756-247-3	US-10-108-260A-1292	US-09-764-853-163	-09-917-800A	-09-764-876-	US-09-764-876-17
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ALIGNMENTS

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Sequence 1810, Application US/0983381
; Bequence 1810, Each IV.
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1el Nu
FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FBSESEQ for Windows Version 3.0
; SEQ ID NO 1810
LENGTH: 3033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1810
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Best Local Similarity 98.0%;
Matches 2648; Conservative
                                                                                                                     1756
1816 ACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGATATTATTTAGGCATG
                                                                                                                                                                                                       1696 GTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACACAGCCTGACTCC 1755
                                                                                                                                                                                                                                                                                  1636 GTTCTAAAAATTCCTGTTCAGCTTGTTTTAAAAAATAAGATAAAGCTATATTGGAGTAAA 1695
                                                                           126
                                                                                                                                                                 66 GTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACACAGCCTGACTCC
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                                                                           ATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAATGCCTCTAATGATATT
                                                                                                    ATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAATGCCTCTAATGATATT 1815
                                                                                                                                                                                                                                                      GTCCGAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAGCTATATTGGAGTAAA
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                                                                                                                                                                                                                                                                                                                                             Score 2584.6;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 3033;
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                                                                                                                                                                                                                                                                                                                                             Indels 51; Gaps
                                                                        185
                              1875
                                                                                                                                                               125
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6 ATGATAAATTTTGCTCAAATATTTACATTTATGATTATCTGACTAAAAAGAACAACTT 1205 6 ACGATAAATTTTGCACCAAAAAGATTATCATTTATGAGGCAAGGTTACCAGAGAGAACATT 2895	6 CCTTACATGACTGACCTGAAAGAGTTCAGATCACTGCAATTGGAGATGTTCTTGGT 1085 6 CCTTCCATCAATGGCTTAACCCTCATTGATTCGGATGCCTTATGGCTGTGACAGAAC 2775 6 CCTTCCATCAATGGCTTAACCCTCATTGATTCGGATGCCTTATGGCTGTGGTGAACAGAAC 2775 6 CCTTCCATCAATGGCTTAACCCTCATTGATTCGGATGCCTTATGGCTGTGGTGAACAGAAC 1145 6 ATGATAAATTTTGCTCCAAATATTTTACATTTTGGATTATCTGACTAAAAAGAAACAACTG 2835	6 ACCCAGATGATTTTAGTANAGGCTGAAGGAATAGAAAATCATATTCACAATCCATCTTA 2591 6	6 CAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTCCCATCAGGCCAACA 2475	6 TTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTTAAGGTAATCATTGAG 235:	176 GTGATCTCTGAGGACCTGGGTCTTGGACTACAACTACTCCAGTGGAGCTCCAAGCCTTC 223	GTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATT 2	186 ACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGAGATATTATTTAGGCATG 245 876 TTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTTGGGTATTGACAGATGCAAAC 193
- Q	p	2	5 B 5 B 7	5 8 8 8	B & B &	. B. & B. &	D Q D Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q
865 TCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGAAGTTAACCTATTAACTGGCTTTATG	2106 TCCGCAAATGGTTTTGGTATTTGCTATTTGTCAAGATGTTGTATATGTGAATGTTAAAGGCT 2165 3745 TCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTT 3804	986 CAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTTCTGATTGACACACAC	B66 AGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCTACTCAAGGATACCACTT 556 GTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATC [33/6 TCATCAGAGTCCAAACTITICTGACTCCTGGCAGCCCCCCTGGCTCCCTGGATATTGAAGTTGCA 3435	256 AAITATACTCTAGCCCTTATAACTTATIGCATTGTCATCAGGGAAGTCCTAAAGCGAAGTTATACTCTATAGCCTTATAACTTATIGCATTGTCATCAGTGGGAAGTCCTAAAGCGAAGTAGCCAATATACTCTAGAAGCGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	136 GTAACACTTACAGCCTATATTGTAACTTCTCTCTGGGATATAGAAAGTATCAGCCTAAC	956 ACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGATCCTTACATAGATATT

361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTAC	241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG	181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT	121 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG	61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA	TGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCTCTGCGTGTGCACCTCCTCTGCGTGTGCACCTCCTCTGCGTGTGCACCTCCACCTCTGCGTGTGCACCTCCACCTCTGCGTGTGCACCTCTGCGTGTGCACC	Query Match 45.9%; Score 1969.4; DB 12; Length 2273 Best Local Similarity 99.9%; Pred. No. 0; Matches 1970; Conservative 0; Mismatches 1; Indels 0;	LENGTH: 2273 TYPE: DNA ORGANISM: Homo sapiens 10-108-260A-953	CURRENT FILING DATE: 2002-03-27 NUMBER OF SEQ ID NOS: 5458 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 953	APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20040005560Aiel full length cDNA FILE REFERENCE: H1-A0106 CURRENT APPLICATION NUMBER: US/10/108,260A	US-10-108-260A-953 ; Sequence 953, Application US/10108260A ; Publication No. US20040005560A1 ; GENERAL INFORMATION:	2706 TGA 2708		4225 CACTCTTCAGTCATTTTTATTTTCTGTTTTCAAGCTTCTGTACTTTATGGAACTTTGGCTG	4165 CTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT	4105 GAGCCAAGGAGACAGGCGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGAG 			3983 AMACICAACCICIATITAGATICIGIAAATGAAACCCAGTTTGTGTTAATA
420 Qy	C 360 Oy 1	300 Oy 365 Db	240 Qy 305 Db	G 180 Qy 1 Db 1 G 245	120 Qy 185 Db	60 Qy 125 Db	; ; Gabs 0; Db	0y Db 1	da Võ	עס ממ	. Qy	Qy bb		TIGGCTG 4284 Db	CCATCAT 4224 Db	CTGTGAC 4164 Db	2525	2465	TCCTGCT 4044 Db
1441 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 1500 	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAACAAGAGATGAAAATATAAAGGTGGGA 1440 	CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT	261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGCAATTCCCAGTCCTGGAGGATTCCAGTGAG 	1 TACTGGAGCGGATCTAACAGTGGAAATCAGAAATTGGAAGCTGTTCAGAAAATAAAT	1141 ACTCTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200 	6 H	1021 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG 1080	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020 	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 	781 AAAGGAGACGTAACGCTTACATTITTACCTTTATCCTTTIGGGGAAAGAAGAAAAATATT 840	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	26 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATATTGTTCT	666 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAACGACCAGACATACTATCAATCA	606 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAAACTTTTCCAGCTATCTTCCCAATA 665 601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGACTGATGACCAGTATTTCAATTTCAATTTCAA	546 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 605 541 TCACAACAACTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600	1 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 5	1 AGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 6 AAGCCAAAAGCAAGAAGTTTTCGCATTTTTTACACTCTTCTCAGATTTTTAAGCCTTAC	426 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA

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APPLICANT: ASTROMOFF, Anna
APPLICANT: BARDAMAN, Olga
APPLICANT: BARDAMAN, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 223
LENGTH: 1300
TYPE: DNA
RORANISM: Homo sapiens
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; OTHER INFORMATION: Incyte ID No.
US-10-133-013-223
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US-10-133-013-223
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Best Local Similarity
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                                                                                                                                                                                                                             Matches 805;
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CAGAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT------
                                                                                     CTACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATA 3598
                                                                                                                                                                       AGGGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTTGCAT 3538
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                                                                CTACTCAGGATACCACTGTGGCTTTAAAGG--CTGTCTGAATTTGCAGCCCTAATGAATA
                                                                                                                                              AGGGAATCCCAATTATGAGGCGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCAT
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                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                            17.0%;
93.6%;
                                                                                                                                                                                                                         Score 730.8; DB 13;
Pred. No. 4.8e-179;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/160,162
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,558
PRIOR FILING DATE: 2001-06-05
PRIOR PILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: COT/US98/15949
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR PILING DATE: 1997-07-30
PRIOR PILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
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                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/10160162 Publication No. US20030166541A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        FILE REFERENCE: PZ012P2
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 83 Human Secreted Proteins
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LENGTH: 875
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,729
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APPLICATION NUMBER: 60/056,561
FILING DATE: 1997-08-19
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APPLICATION NUMBER: 60/054,213
FILING DATE: 1997-07-30
APPLICATION NUMBER: 60/055,968
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APPLICATION NUMBER: 60/055,969
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FILING DATE: 1997-07-30
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                                                                                                                                                                                                                                                                             CGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGG 3925
                                                                                  TGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATG 4105
                                                                                                                           AACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCTG
                                                                                                                                             AACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCTG 4045
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AGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACC
                    AGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACC 4165
                                                            TGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATG
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Pred. No. 6.4e-130;
1; Mismatches 0;
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; ORGANISM: Homo
US-09-820-649-48
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: PZ012P1
FULE REFERENCE: PZ012P1
CURRENT APPLICATION NUMBER: US/09/820,649
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US/09/236,557
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
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US-09-820-649-48
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SEQ ID NO 48
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Matches 541;
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Best Local Similarity
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Publication No. US20030199683A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,211
PRIOR FILING DATE: 1997-07-30
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PRIOR TILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
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                                 TGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTGGAATATGATCATGGAA 3985
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Pred. No. 6.4e-130;
1; Mismatches 0;
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FEATURE:

NAME/KEY: unsure

LOCATION: (285)

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US-09-360-352-12867
Sequence 12867, Application
; Patent No. US20020137139A1
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LENGTH: 354
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Best Local Similarity
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APPLICANT: Tao, Nenghing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(30298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 354
TYPE: DNA
ORGANISM: Bos taurus
                                                                                      2264
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                                                                        CCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGA 2323
AAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGA 2383
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                                                      CATACTCTGTCATCAGAGGTGAAGAATTTGCTTTGGAAGTAACCATATTCAATTATTTGA
                                                                                                                                                                                              ATTCTATCACTTCTTGGGTTGCAACTGCTTTTGTGATCTCTGAGGATTTAGGTCTTGGAC
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                                                                                                                           TAACAACTGCTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTTGAATCTTC
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Pred. No. 5.1e-60;
0; Mismatches 36
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US-10-027-632-204326/c
US-10-027-632-204326/c
; Sequence 204326, Application US/10027632
; GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

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PRIOR APPLICATION NUMBER: US 60/146,002
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US-10-027-632-204326/c
US-90-27-632-204326, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-204326
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SOFTWARE: FastSEQ for Window
SEQ ID NO 204326
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TTTGCATCTACTCAGG
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Pred. No. 1.3e-39;
0; Mismatches 1;
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; SEQ ID NO 204326
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-204326
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US-10-316-253-266
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      Query Match
Best Local Similarity
Matches 575; Conserv
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                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 4677
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                                                                                NAME/KEY: CDS
LOCATION: (52)..(4554)
OTHER INFORMATION:
-10-316-253-266
                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating
FILE REFERENCE: 8065M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: PastSEQ for Windows Version 4
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PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
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                                                                                                                                                              TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                FEATURE:
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FILING DATE:
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ilarity 47.3%;
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Pred. No. 3e-22;
0; Mismatches 590;
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Pred. No. 1.3e-39;
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GTGATTCATAGTGAGCTTCAAGGTGGCAATAAAAGTCCAGTAACACTTACAGCCTATATT 3156
                                                                                                                     TTAAGATGTTTTCCTTGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGA
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                              GCTTTCAATTGGCTCTCGATGAAACAAAGGGAGAACGGTTGTTTCCAACAGTCTGGATCC
                                                             ACATACACTTGGCTTAAAGGACATCAGAAATCCAACGGTGAATTTTTGGGATCCAGGAAGA 3096
                                                                                               CTCAAGGCCTTCGCTCAAGCTCAGTCATACATCTATATAGAAAAGACACACATCACAAAT
                                                                                                                                                              ACATTCGGGGACCGCGTATGAGGCACAGTCAGGGAAACACTTGGCTCACTGCATTTGTG
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; LOCATION: (95)..(4597); OTHER INFORMATION: US-10-316-253-268
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US-10-316-253-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 268, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Procter & Gamble Company APPLICANT: Peters, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
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NAME/KEY: CDS
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Local Similarity 47.3%;
nes 575; Conservative
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                                                                                               TCAAGTGAAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCCAGTGAGGATGGG 2445
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       GCAACTGTTCTTTTTCCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACA 2505
                                                    GGAAATGAAAGAAAAACCGTGTCCTGGGCTGTGACCCCAAAGTCGCTGGGGGAGGTGAAC
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Greis, Kenneth
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b. US20030162706A1
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
ITITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-07-10-05
PRIOR FILING DATE: 2000-10-06
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                                                                                                                                                                                                                                                                                                                                                         US-09-880-107-3727
                                                                                                                                                                                                                                                                                Sequence 3727, Application Patent No. US20020142981A1 GENERAL INFORMATION:
                                                                                                                                                                                       APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, In
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SOFTWARE: PATENTIN VEY:
SEQ ID NO 3727
LENGTH: 4615
TYPE: DNA
                                                                                                                                                                            Sequence 405, Application US/10006285 Publication No. US20030165854A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 318; Conserv
SEQ ID NO 405
            APPLICANT: Mary Jane Cunningham
APPLICANT: Matthew R. Kaser
TITLE OF INVENTION: MARKER GENES RESPONDING
FILE REFERENCE: PA-0039 US
CURRENT APPLICATION NUMBER: US/10/006,285
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 514
SOFTWARE: PERL Program
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APPLICANT:
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APPLICANT:

MacDougall,

Muriel M

Gerlach,

Valerie

Malyankar, Muriel N Smithson, Glennda Millet, Isabelle Peyman, John A Stone, David J

APPLICANT: APPLICANT:

Shimkets, Richard Gunther, Erik Ellerman, Kare

APPLICANT:

Sequence 9, Application US/09981151A
Publication No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R

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RESULT 13
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Best Local Similarity
Matches 318; Conserv
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TYPE: DNA
ORGANISM: Homo:
FEATURE:
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OTHER INFORMATION:
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Pred. No. 2e-21;
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CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
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TITLE OF INVENTION: Proteins and Nucleic Acids
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APPLICATION NUMBER: 60/242,881
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APPLICATION NUMBER: 60/242,612
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APPLICATION NUMBER: 60/241,040
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                               CCTGGCTAAATCGCATGAGTACCAGCTAGAATCATGGGCAGATTCTCAGACCTCCAGTTG
                                                                CATTGAGAAAA-
                                                                                              CTTTCGTCTTACTGCCACCATCTTCAATTACCTAAAGGATTGCATCAGGGTTCAGACTGA
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Spytek, Kimberly A
Gangolli, Esha A
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Guo, Xiaojia
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Taupier Jr, Raymond
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Spytek, Kimberly A. Patturajan, Meera Tchernev, Velizar T Liu, Xiaohong

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LOCATION: (1)..(4309)
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TYPE: DNA
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CURRENT FILING DATE: 2002-03-07
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PRIOR FILING DATE: 2001-03-08
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APPLICATION NUMBER: 60/288,052
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FILING DATE: 2001-08-17
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APPLICATION NUMBER: 60/274,194
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APPLICATION NUMBER: 60/274,281
FILING DATE: 2001-03-08
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Rastelli, Luca
Spaderna, Steven
LaRochelle, William
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; LOCATION: (1119)
; OTHER INFORMATION: n equals a,t,9, or
US-09-764-853-362
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US-09-764-853-362
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PATENT NO. US2002090672A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
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Best Local Similarity
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NAME/KEY: SITE
LOCATION: (1018)
OTHER INFORMATION: n equals a,t,g,
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TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: January 17, 2004, 00:35:05 Job time : 1346 secs

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JOURNAL MEDLINE	TITLE	AUTHORS	PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION				DEFINITION	Locus	AK029247	RESITT 1
prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	10349636	99279253	Meth. Enzymol. 303, 19-44 (1999)	High-efficiency full-length cDNA cloning	Carninci, P. and Hayashizaki, Y.	44	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)	HTC; CAP trapper.	AK029247.1 GI:26081244	AK029247	sequence.	alpha-2-macroglobulin (fragments) [Limulus polyphemus], full insert	library, clone:4831440K17 product:weakly similar to	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched	AK029247 4485 bp mRNA linear HTC 05-DEC-2002		

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                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Pax:81-45-503-9216
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4485)
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                           Division of Experimental Animal Research
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FEATURES
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Best Local Similarity
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ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCAGGGCCCACCGCTCCTGACCGCCCCCCCCTCCTCTGCGTGTGCACCGCCGCCTG
                                                                                                     GITTCAGAATAIGIATIACCAAAAITIIGAAGIGACTTIIGCAGACACCATTATAIIGITCI 720
                                                                                                                                                                                 TCACAACAAAGTGATCTTGGAGTCATTTCCCAAAACTTTTCAGCTATCTTCCCAATCCAATA
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                                                                     GTCCTAGAATATGTGTTACCAAAGTTCGAAGTCACCGTGCAGACCCCGCTGTATTGTTCC
                                                                                                                                                          TTTGGTGACTGGTCCATTCAGGTTCAAGTGAATGATCAGCAATATTACCAGTCATTTCAG
                                                                                                                                                                                                                                                  TCTCAGAAAGGTGATCTTGGAGTCGTTTCCAAAACTTTTCAACTATCCTCTAATCCAATA
                                                                                                                                                                                                                                                                                                                                         AGGACATCCGTGGACATTTTCATTAAGGATCCGAAGTCTAATGTGATCCAACAGTGGTTT
                                                                                                                                                                                                                                                                                                                                                                AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //note="putative
//note="putative
weakly similar to alpha-2-macroglobulin (fragments)
[Limulus polyphemus] (PIR|A36260, evidence: FASTY,
51.8%ID, 76.7%length, match=168)"
a 970 c 1010 g 1228 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="0 day neonate" 112. .4439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="head"
/clone_Tib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="4831440K17"
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Pred. No. 0;
0; Mismatches
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1839 TCTCTCÁGÁTCTCTGCÁCÁCÁGTCTGÁCTCCTGGTGGGÁTTGTÁGCTGTTGÁCÁÁA 1898 1783 AGTGTGAATCTGATGAATGCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTG 1842 1783 AGTGTGAACATTGATGAAAACCTCCAACAGTATTACAATGGAAAACCATGGTCCATGAACTG 1958	1779 TTTGAAAATAAGGTAAAGCTGTTTTGGAGTAAACCTACAGTCAAGCCATCTGATAAGGTC 1838 1723 TCTCTTAGGATCTCTGTGACACAGCCTGACTGCCATAGTTGGGAGTTGTTGACAAA 1782	1603 TATATTGAAGATGATGAGGAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTT 1662	1543 ACAATGTTCTCTTTAACACCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTAT 1602 	GAGTTAAGCTATATGGTAGTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCA	GAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAG 		1303 CTGGAGGATTCCAGTGAGCTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATG 1362	1243 GTTCAGAAAATAAATTATACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATC 1302 		1123 GCTGATGGCAACCAACTGACTCTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACA 1182 		1003 TCAAGAAATGTAAGCACTAATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTT 1062	943 CTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTAAT 1002	901 AATGTAATGARTTCTTCAAATGGACTTTCTGAATACCTGGAT 942	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 	781 ANAGGAGACGTAACGCTTACATTITTACCTTTATCCTTTTGGGGAAAGAAGAAAATATT 840
2863 TCATTTATGAGGCAAGGTTACCAGAGAAACTTCTCTATCAGAGGGAAGATGGCTCTTTC 	DD 2859 AICCGGAIGCCTATGGAIGTGGTGAACAGAACATGATATTTTGCTCCAAATATTTAC 2918 QY 2803 AITTTGGAITATCTGACTAAAAAGAAACAACTGACAGATAATTTGAAAGAAA	2799 GTTCAGATCACAGCAATTGGAGAACATGATCATTTTAC 2791 ATTCGGATGCCTTATGGCTGGTTGAACAGAACATGATAAATTTTACCTCCAAATATTTAC 271 ATTCGGATGCCTTATGGCTGGTGAACAGAACATGATAAATTTTACCTCCAAATATTTAC 271 ATTCGGATGCCTTATGGCTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTAC	2623 AGTACCCTGAAAACTTTGAGTTTCTCATTTCCCCTAATACAGTGACTGGCAGTGAAAGA	2563 GGAATAGAAAATCATATTCACAATCCATCTTATTAGACTTGACAATAGGCTACAG 	Qy 2503 ACAGCTCTTTCACCCACTGCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAA 2562	QY 2443 GGGCCAACTGTTCTTTTTCCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTC 2502	QY 2383 ACTTCAAGTGAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGAT 2442	QY 2323 AAAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAAGTGACAAATTTGATATTGTAATG 2382	Qy 2263 CCCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTG 2322	QY 2203 CTAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTT 2262	Oy 2143 GATICTATCACTICTTGGGTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGA 2202	Qy 2083 ATTTGGCTAGACACCAACATGGGTTACAAGAATTTGAAGTAACTGTACCT 2142	Qy 2023 ATTCATGACTTTTCTTTGGGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGG 2082	1963 TATGA 2079 TACGA	1903 GAATG 2019 GAATG	1843 GAACTTTATAACACAGGATATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAG

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                                                                 CTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGC
                                                                                                                                                      AATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCT
                                                                                                                                                                                                                ACCGAAAATCAAGAAGTTTTTGATTTAGACGTCATTGTGA---ATAATGAGGACGACATT
                                                                                                                                                                                                                                      ATCCAAAATCAAGAAGCCTTTGATTTTAGATGTTGCTGTAAAAAGAAAATAAAGATGATCTC
                                                                                                                                                                                                                                                                                                                              TGTCAGCTCAATGTTGTATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCT
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                                      CTTATGGAAGTGAACCTTCTCAGTGGCTTTAGTGCATCTTCAGATTCAATTCCTCTGAGT
                                                                                                                           AGT CACCTGAATCTGAATGTGTGCACAAGTCACTTGGGTTCAGAGAGGACAGGCATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site for further details.
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                                                                        AAGCTACAACACCCAGGTGAAGCTGTCCTCGTGTTACCT---CAGTCCAGACACCAACTG
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On Feb 15, 2001 th:
Contact: Genoscope
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cgi-bin/cluster.cgi?seq=CSODIOsDA09QPl&cluster=3578.f.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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a 238 c 236 g 293 t 75 others
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
                                                                         Mammalia, Eutheria, Primate
1 (bases 1 to 941)
Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
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Mammalia; Eutheria;
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more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAND29ZD07 CSO2740_1&cluster=3578.f.
Contact : Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAND29ZD07_CS02740_1.
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the POWSPORT 6 vector. Library was normalized.
a 214 c 181 g 266 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI081YB18"
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5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14090 row: p column: 10
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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TATGCTGACTTGGAGAGCAGAACAAGAAGGTGGCATGCAATTCTGGGTGTCATCAGAGTC
                                                      AGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTTCAGACAATTATACTCT
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                                                                                             AGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTTCAGACAATTATACTCT
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                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 663.
                                                                                                                                                   Conservative
                                                                                                                                                                                                               /clone="IMAGE:6514905"
/tissue type="leiomyosarcoma"
/lab_host="DH108 (phage-resistant)"
/clone lib="NIH MGC_71"
/clone="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb. "
a 171 c 206 g 253 t 1 others
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/mol_type="mRNA"
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Pred. No. 3e-147;
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                                                                           AGCAATTTCTCCTGAGCGAGACAGTGAGGAAAGTGGGGATATGATCATGGGAAAACTCAAC
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REFERENCE AUTHORS TITLE COMMENT JOURNAL

BX386457 Homo sapiens PLACENTA COT 25-NORWALIZED Homo Clone C50DI081YB18 5-PRIME, mRNA sequence. clone CS0DI081YB18 BX386457 BX386457.1 GI:30457430 sapiens

EST

Homo sapiens (human

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

and Polayes,D. d normalization

Eukaryota; Metazoa; (
Eukaryota; Metazoa; (
Mammalia; Butheria; I
1 (bases 1 to 978)
Li.W.B., Gruber, C., (Full-length cDNA libraries and Unpublished

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f

For

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGAAATGTG
GAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCTATGAAT 726
                                                                                                                                                                                                                                                      TCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTGTCACAA 546
                                                                                                                                                                                                                                                                                                                                         AAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTACAAAACC 486
                                                                                                                                                                                                                                                                                                                                                                                                        TCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAGCCA 426
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                                                                                     CAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATACTTGGT
                                                                                                                                                                              CAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATACTTGGT 606
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/mol type="mRNA"
/mol type="mRNA"
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/db_xref="taxon:9606"
/clone="CSODIO81YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib" strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed double-strand cDNA was
/primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
74 a 151 c 179 g 220 t 54 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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UI-H-CO0-arh-c-08-0-UI.sl NCI_CO
IMAGE:3106526 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                           194
                                                                                                                                                  Carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI CGAP Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TAGC, TAACC, ATGG, AGACA, ATCAC. For additional divisions of the contains a library are contained by the contains a library are CGTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP Sub9"
/clone lib="NCI CGAP Sub9"
/notee="Vector: pT713-Pac (Pharmacia) with a modified
/notee="Vector: pT713-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
                                                                           TAG_LIB=UI-H-CO0
TAG_TISSUE=Cervical Adenosquamous Carcinoma
                                                                                                                                 information,
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/mol_type="mRNA"
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                                                                                                                                    bento-soares@uiowa.edu
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Unpublished
On Feb 16, 2001 this sequence version replaced
Contact: Genoscope
Genoscope - Centre National de Sequencage
                                       Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                           AL576908 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CSODIO81YB18 3-PRIME, mRNA sequence.

AL576908 AL576908 GI:31315187
EST.
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                                                                                         Homo
                                                                                                   Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                            GGTTGTCACAACAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATC
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Pred. No. 3.1e-135;
Pred. No. 3.1e-135;
                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was Constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO81DA09NP1&cluster=3578.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO81DA09NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTCTGAATTTGCAGCCCTAATGAATACAGAAAAGGACAAATATCCAAGTGACCGTGACG
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                                                                          AACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCA
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AGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCCATCATCACTCT
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the PCMVSPORT 6 vector. Library was normalized."
a 248 c 224 g 321 t 64 others
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/db_xref="taxon:9606"
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Pred. No. 2.9e-133;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSJA1021ZB10NP1&cluster=3578.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AI021ZB10NP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
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988 bp mRNA linear EST 08-MAY-200:
BX386456 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens cDNA clone CS0DI081YB18 3-PRIME, mRNA sequence.
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AGTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCA 3939
                                                                                                                                                                    AGACGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAAT 3819
                                                                                                                                                                                                                                                              GGATTTGCTATTTTGTCAGCTCAATGTTGTATATAATGTGAAGGCTTTCTGGGTCTTCTAGA 3759
                                                                                                                                                                                                                                                                                                                                                              TCACCAAGTCCTCTTGCTGTGGTACAGCCAATGGCAGTTAATATTTTCCGCAAATGGTTTT 3699
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                                              AAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAATCTTTTCNNNCCC-GNTANT
                                                                                     AAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCCGGGTAGG 3879
                                                                                                                                         AGACGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAAT
                                                                                                                                                                                                                                      GGATTTGCTATTTGTCAGCTCAATGTTGTATATAATGTGAAGGCTTSTGGGTCTTCTAGA
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/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Nomo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 133 c 164 g 249 t 58 others
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/mol_type="mRNA"
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Pred. No. 3.6e
12; Mismatches
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UI-H-FG1-bgj-1-22-0-UI.s1 NCI CGAP FG1 Homo
UI-H-FG1-bgj-1-22-0-UI 3', mRNA sequence.
BU624356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 638)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       upr. M. Bento Soares, bento-soares@uiowa.edu primer: M13 FORWARD
                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/mb xref="taxon:9606"
/db xref="taxon:9606"
/clone="U1-H-FG1-bg]-1-22-0-UI"
/clone="U1-H-FG1-bg]-1-22-0-UI"
/tissue_type="Cell lines"
/dev stage="Adult"
/lab host="DH108 (Life Technologies)"
/lab host="DH108 (Life Technologies)"
/lab host="DH108 (Life Technologies)"
/clone_lib="NCI_CGAP_FG1"
/clone_lib="NCI_CGAP_FG1"
/more="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
/more="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FG1 is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Index
The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-80, First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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RESULT 11
AA418644
LOCUS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                   sequence.
AA418644
AA418644.1
EST.
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 634)
Hillier,L.; Allen,M., Bowles,L.,
                                                                                                                                                                                       AA418644 634 bp mRNA linear zv93f07.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone similar to TR:G534873 G534873 ALPHA-2-MACROGLOBULIN.
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                           Homo sapiens
                                                                                               Homo sapiens (human)
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TAG_TISSUB-Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ=CGGTCACTC*
TAG_SEQ=CGGTCACTC*
139 c 109 g 187 t
                                                                                                                                     GI:2080463
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Pred. No. 1.3e-114;
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IMAGE:767365 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
GGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATT 3942
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                                                                                                                GTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCTCTGTGACCTTTGCAGTGATGTCCAG
                                                                                                                                                                                                                                                                                                              GATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCTGTGAGAAACTTTAAAAGTT
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                                                                            GTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAG
                                                                                                                                                                                                                     TCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAGGAGACAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Soares NhHMPu_S1"
//clone lib="Soares NhHMPu_S1"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
74 a 109 c 139 g 212 t
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pregnant uterus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:767365"
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Pred. No. 1.2e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sequences. Mamm.
Please visit our web site (ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno, H., Fukknishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, T., Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carninci, P., Sugara, Carnin
                                                                                                                                                                                                                                                                                                                                                                                                further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTTCTGTTTCAAGCTTCTGTACTTTATGGAACTTTTGGCTGTGA 4287
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/sex="mixed"
/tissue_type="head"
/dev_stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                       /db_xref="taxon:10090"
/clone="4832419I01"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                   organism="Mus musculus"
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2585 AATCCATCTTATTAGACTIGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTGAGTT
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                                                                                       ATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCCTGGGATATAGAAAGT 3184
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                                                                                                                                                                            AATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGTGGCA 3124
                                                                                                                                                                                                                                                                        ACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACATCAGA 3064
                                                                                                                                                                                                                                                                                                                                                                CTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTTCCTTGAAGCCGATCCTT 3004
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K-EST0217654 L18POOL1n1 F
5', mRNA sequence.
CB158337
CB158337.1 GI:28143473
EST.
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1 (bases 1 to 613)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kin Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. Kim,Y.S.
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Plate: 10 row: H column: 06
High quality sequence stop: 613.
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                                                                                                                                     CTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGC
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/note="Organ: Liver, Vetcor: pT7T3-Pac; Site_1: EcoRI;
/note="Organ: Liver, Vetcor: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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/cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10F'"
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DKFZp686C02145_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686C02145_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Lt
Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        el sequence also available.
This clone (DKFZp686C02145) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker, H., Boecher, M., Mewes, H.W., Fobo, G., Han, M. and Wiemann, S.
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1 (bases 1 to 515)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAG-ATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAG 4130
                                   AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTACAACTCTGAAGTGAAGCTGTCCTCCTG 4160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGAAACCCAGTTTTGTGTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACC
                                                                                                                                                   ATGCAGGGCCCACCGCTCCTGACCGCCCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG
                                                                                                                                                                                      ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAG
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                                                                                                                                                                                                                            Conservative
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Pred. No. 3.3e-99;
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                                                                                                                                                                                                                                                              Length 515;
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199
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AUTHORS
TITLE
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BX370169
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VERSION
                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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    Query Match 11.5
Best Local Similarity 94.4
Matches 577; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAGO38ZHO4_CSO3584_1&cluster=3578.f.
Contact: Feng Liang Email: filang@lifetech.com UTL:
http://fulllength.invitrogen.com/ InVitroGen Comporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAGO38ZHO4_CSO3584_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919 bp mRNA linear EST 08-MAY-200:
BX370169 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens cDNA
clone CS0D1081YB18 5-PRIME, mRNA sequence.
BX370169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX370169.1 GI:30455906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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sites of the pCMVSPORT 6 vector. Library was normalized."
85 a 213 c 177 g 242 t 2 others
                          11.5%;
Score 493.8; DB 13; Length Pred. No. 1.1e-98; O; Mismatches 27; Indels
                                                   919;
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722 TGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTGA 781

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; AGTGAGCTACA 1325 AGCGAGCCTCA 614	A-TACTGTCCCCCAAAGTGGAACTT-TTAAGATTGAATTCCCAATCCTGGAGGATTCC	AGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	TGACTCTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTG	GAAGCCATCTCAACTTCACAGCCA-CTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTA-CTGTCTT	GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT	ATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	CAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAAA	AAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAGAAAATATTA	
	1314 603	1258 543	1198 483	1138 423	1079 363	1020	960 243	901 183	841 123	L

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Search completed: January 16, Job time: 7735 secs

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SOURCE ORGANISM

Homo sapiens Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS TITLE JOURNAL

Schuh, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides Patent: WO 02070696-A 1 12-SEP-2002;

and methods

VERSION KEYWORDS

AX534934.1

GI:25261474

RESULT 1
AX534934
LOCUS
DEFINITION
ACCESSION

4761 bp Sequence 1 from Patent WO02070696.

DNA

linear

PAT

22-NOV-2002

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 0 0 0 0 0 0 a a ဂ .4219.8 3187.4 3185.8 2709.2 2448. 152.2 151.2 149.8 146.4 143.8 143.8 143.8 143.8 143.8 143.8 143.8 136.8 203.8 182 177.4 175.174 174 174 171.6 167.6 730.8 232 230 219.6 1969.4 Score Match Query 98.5 98.4 98.4 74.4 74.3 63.2 63.2 57.1 17.0 7.0 1300 5.4 163577 5.4 176144 5.1 5603 4.8 4678 4.2 251250 4.1 91419 4.1 149597 3.4 4950 3.4 122013 3.4 164414 3.4 168503 3.4 275699 3.4 337178 3.3 191258 4620 176144 4579 144589 191258 Length 4560 2629 4715 4578 4636 В AC012408) RATA113A DME269538) GPIMSPB) RATA113 GGOVOM AY122084 DME269539 AC112668 AC118254 PRNA113 AC118254 BC036299 BC051037 AB026130 AC092399 AC092395 AC115484 AE003649 DROSADH08 D83196 AC097023 AL591480 AC034271 AX054953 AX054954 AY118302 AX534944 AY083458 BC052443 HSM805581 AK095888 AC012408 CIN431688 AX534940 AX537610 AX537612 AX534934 AF410459 XELENDO AL590428 AX083146 AX534936 ALIGNMENTS AXOB3146 Sequence AXS90428 Human DNA AC012408 Homo sapi AJ431688 Ciona int D83196 Limmlus sp. AC097023 Rattus no AL591480 Human DNA AC034271 Homo sapi AX054953 Sequence AX054954 Sequence AX054954 Sequence AX118302 Drosophil X78801 G.gallus mR AX122084 Drosophil X782084 Drosophil AJ269539 Drosophil AC112668 Mus muscu AC11854 Mus muscu X52984 Rat mRNA fo AC012508 Homo sapi J03552 Rat plasma AJ269538 Drosophil L63543 Xenopus lae AC092399 Drosophil AC092395 Drosophil AC115484 Drosophil AE003649 Drosophil AE003414 Drosophil AE003414 Drosophil AC118254 Mus muscu BC036299 Mus muscu AX537612 Sequence AX534942 Sequence AX534944 Sequence AY083458 Mus muscu BC052443 Mus muscu AL834478 AK095888 AX534934 AF410459 Description AB026130 Cyprinus D84339 Cavia porce J03524 Rat alpha-1 Ното варі Ното варі Sequence Sequence Sequence Sequence

Minimum Maximum

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Total number of hits satisfying chosen parameters:

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IDENTITY_NUC .
Gapop 10.0 , Gapext 1.0

US-10-020-095-3 4287

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January 16, 2004, 12:38:20 ;

; Search time 14986 Seconds
(without alignments)
11702.894 Million cell updates/sec

Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45

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Database

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å å	B 8	DB Q	ОУ	B 8	B &	B 8	gb Qy	Query Match Best Local : Matches 428	BASE COUNT ORIGIN								- CDS	FEATURES source
421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC 480	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC 360	241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300 	181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGGAGAAGGAGTCTTT 240	121 AATGTGACTATTGGGGTGGAAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 180	61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA 120	1 ATGCAGGGCCCACCGCTCGTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCGCTG 60	Query Match 98.5%; Score 4224.4; DB 6; Length 4761; Best Local Similarity 98.8%; Pred. No. 0; 4450 Matches 4286; Conservative 0; Mismatches 1; Indels 51; Gaps 1;	TLYENGERING G 1413 t 1420 a 912 c 1016 g 1413 t	YALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTN IQVTVTGPSSPSPVKFLIDTHNRLLLQTAELAVVQPMAVNISANGFGFAICQLMVVYN VKASGSSRRRRSIQNQEAFDLDVAVKENKDDLMRVDLMVCTSFSGPGRSGMALMEVNL LKGFMVPSEBAISLSETVKKVENYDHKKLMLYDSVNETQFCVNIPAVRNFKVSNTQDAS	IRMPYĞCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDĞ SFSAFGNYDPSGSTMLSAFYLRCFLEADPYIDIDYQNLHRTYTMLKGHQKSNGEFMDP GRVIHSELQGGNKSPVTLTAYIUTSLLGYRKYQPNIDVQESIHFLESEFSRĞISDNYT LALLIYALSSVGSPKAKEALNMLTMRAEDGRGMQFWYSSESKLSDSMQPRSLDIEVAA	SPHVRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPV ELQAFQPFFJFLALPSSULFGIRFTTFFVIKTALSEPTASDAVTQMILVKAEGI INATGHQQTLLVPSEDGATVLF9IRPTHLGEIPITVTALSPTASDAVTQMILVKAEGI EKSYSOLJLLVFSEDGATVLFFIRFTHLGEIPITVTGSERVQITALGDYLQFSINGLASL	KSSMAVHSLEKS PSKTY I QLKTRIDEN I KVOSPFELVVSCHKELKELYMVSREGOLVA VGKQNSTMFSLT PENSMT PKACVI VYY I EDDGEI I SDVLKI PVQLVFKNKI KLYWSKV KAEFSEKVSLRI SVTQPDS I VGI VAVDKS VILMARAND I TMENVVHELEL YNTGYYLG MFMASFAUFOFGI, MVI, TDANI, TRIVYI DANEY PRESPMERMENFH I VDI THPSI IGS	FOUSEYLLERGE NORMAL SCHOOL TEXTS TO THE STATE OF THE STAT	/tzanslation="MQGPDIJTAAHLLCVCTAALAVAPGPRFLYTAPGIIRPGGNVTI /tzanslation="MQGPDIJTAAHLLCVCTAALAVAPGPRFLYTAPGIIRPGGNVTI GVELLEHCPSQVTVKAELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY ELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYKEKGEVKFRIVTLFSDFKPY KTEINLIKTPBKRJLJONNISSPENGRIVTGKTEITGTNSTATOTONNNOTVYOG	<pre>/note="unnamed protein product" /codon start=1 /proteIn_id="CAD57231.1" /db xref_mcI.35261475"</pre>	/organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606" 1134450	Schuh, And L 1
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Homo sapiens CD109 (CD109) mRNA,
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AF410459.1 GI:19071208
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Submitted (14-AUG-2001) Medicine,
College Circle, Room 7366, Toront
                                                                                             Lin,M., Sutherland,D.R.,
Wu,X.-F. and Schuh,A.C.
                                                                                                                                                                              Cell surface antigen CD109 is a novel member of the alpha(2) macroglobulin/C3, C4, C5 family of thioester-containing proteins Blood 99 (5), 1683-1691 (2002)
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RESULT 3 AX534938 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
AX534938 AX534938 Sequence 5 from Patent W002070696. AX534938 AX534938.1 GI:25261482 Homo sapiens (human) Homo sapiens Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Schuh, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides and methods of use Patent: W0 02070696-A 5 12-SEP-2002; Schuh, Andre-(CA) — Sutherland, Robert D. (CA) Location/Qualifiers 1. 5895 Corganism="Homo sapiens" /mol_type="genomic DNA"	3601 GAANGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT

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Query Match Best Local Similarity Matches 4285; Conserv 661 601 653 541 593 481 533 421 473 361 413 301 353 293 173 113 773 713 241 181 233 121 5 -ATGCAGGGCCCACCGCTCCTGACCGCCGCCCCCCCCCTCTGCGTGTGCACCGCCGCGCGTG GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAAGTGATCTTGGAGTCATTTCCCAAAACTTTTCAGCTATCTTCCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGA GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT CTTGGTGA ANAACCTCTTTAAACATTCTCATTAAGGACCCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG ATGCAGGGCCCACCGCTGCTGACCGCCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG Conservative 98.5%; 0 Score 4222.8; Pred. No. 0; Mismatches BB 2; 6, Indels Length 4761; 51; Gaps 532 472 120 832 720 772 660 712 600 652 540 592 480 420 360 412 180 232 172 60 300 352 240 292

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Db 2813 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAACATTTTGATTCGGATTCCTTATGGC 2872 Oy 2761 TGTGGTGAACAGAACATGATTATTTGCTCCAAATATTTTACATTTTGGATTATCTCTCCACT Db 2873 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTTGGATTATCTTGACT OY 2821 AAAAAGAACAACTGACAGATAATTTTGCTCAAATATTTTACATTTTATGAGGCAAGGT 2880	GETTCTGATTCCTCCTAATACAGTGACTTAGCCTCATTGATTCAGATTCCTGATGCCTTATTCACAATGCCTTAATACAGTAAAGCTTAAGAAAAAAACTTTG	2453 AAGGTAATCATTGAGAAAAATTGACAAAATTCAACAGCTCTTTCACCCACTTTCACCCACTTCACCCACTCACCACC	Db 2273 ĠTĠĠĊTÁCTĠĠŤTTTĠTĠĂTĊŤCTĠĀĠĠĂĊĊŤĠĠĞTĊŤTĠĀĊŤĀĊŤĀĊŤĠĊĞĠŤĠ 2332 Qy 2221 GAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA 2280 Qy 2231 GAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGA 2392 Db 2333 GAGCTCCAAGCCTTCCAACCATTTTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGA 2392 Qy 2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTTGAATTATTTGAAAGATGCCACTGAGGTT 2340	2041 GGTAGCAGTCCACATGTCCGAAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCCAAC	Qy 1801 GCCTCTAATGATATTACAATGGAAAATGTTGGTCCATGAGTTGGAACTTTATAACACAGGA 1860

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KEYWORDS REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM RESULT 5 AX534940 FEATURES source SGS AX534940 5895 bp Sequence 7 from Patent WO02070696. AX534940 AX534940.1 GI:25261486 Homo sapiens (human) Schuh, A. and Sutherland, R.D. Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; nucleic nucleic acid molecules polypeptides : WO 02070696-A 7 12-SEP-2002; Andre (CA) ; Sutherland, Robert D. Location/Qualifiers /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 113. .4450 1. .5895 note="unnamed protein product" Craniata; Vertebrata; Catarrhini; Hominidae; DNA and Hominidae; (S linear methods PAT Euteleostomi; Homo 0f 22-NOV-2002 use

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TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1	Q ¦	Db 833 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 892	
1801 GCC ICIANIGATA ITA LA ISSAMANTI GIGGI COLIGNOI I GANACII II ITANCACAGGA 1888 18	D &	OY 721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	
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191 CHAMACHI I LIBERT COMMENCE GEGERATION GEGERATION GEGERATION (1918) 1910 1910 1910 1910 1910 1910 1910 191	מם	OY 481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	
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LALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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	3421 GATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTTCTTACAATTTCAGACTTCTGAG 3480	
ORGANISM	-	
ACCESSION VERSION KEYWORDS	3361 ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTG 3420	
RESULT 8 AX534942 LOCUS DEFINITION	3301 AGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGCAGAACAAGAAGGTGGC 3360 	
43	3241 AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCATTGTCATCAGTGGGG 3300	
Db 426 Qy 427		
Оу 421	81 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGT	
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Оу 403	01 C. LEACUAGA WALLIA CAN TAN TAN TAN TAN TAN TAN TAN TAN TAN T	
Db 402	2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3000 	
Qy 397	B81 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTTGGGAATTAT 2	
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Qу 391	821 AAAAGAAACAACIGACAGATAATITIGAAAGAAAAGGTCTITICATTTATIGAGGCAAGGT 28	
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	41	
Db 366	81 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG 264	
Οу 365	5.81 ТСЭСЭЭТССЭТСТТЭТТЭСЭСТТСЭСТЭСЭЭТЭСЭСТЭССТЭССТЭСССТЭСССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭССТЭСС	
Db 360		
0у 360		
Db 354	2461 CCCATCAGCCCAACACACACACAAAAATTCCCTATCACAGCCACACACA	
Оу 354	01	
Db 348	01 GCCACAGGCCAGCAGACCCTTCTGTTTCCCAGTAAGAATGGGGGAACTGTTCTTTTT 246	
Оу 348		

음 성

REFERENCE

Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

AX534942 3535 bp Sequence 9 from Patent WOO2070696. AX534942 AX534942.1 GI:25261490

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linear PAT 22-NOV-2002

			RESULT 8
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	ATGGAACTTTGGCTG 4284	4270	δ
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3960	GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA	3901	DЬ
3909	GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA	3850	ş
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3729	ATGGCAGTTAATATTTCCGGCAAATGGTTTTGGATTTGCTATTTGTCAGCTCAATGTTGTA	3670	ş
3720	CTGATTGACACACAACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA	3661	Дb
3669	CTTGCTGTACAGCCA	3652	Ş
3660	GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTT	3601	DЬ
3651	GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT	3601	Ş
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3540	GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT	3481	γQ

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	OY 241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300
61	QY 181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGGAGGAGTCTTT 240
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1141 ACTOTTGAAGAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 	OY 61 GCCGTGGCTCCCGGGCTTCCGGTTACAGCCCCAGGGATCATCAGGCCCCGAGGA 120
1081 ARGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	Db 13 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCTCTGCGTGTGCACCGCCGCTG 60 Db 13 ATGCAGGGCCCACCGCCCCCCGCCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG 172
1021 AARGTGTTCTTCAAGCAACATGATTACATGAGTTTTTGATTATACTACTGTCTTG	Query Match 74.4%; Score 3187.4; DB 6; Length 3535; Best Local Similarity 100.0%; Pred. No. 0; Matches 3188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	ELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSNE Qy INATGHQQTLLVPSEBGATVLFPIRFTHLGEIPITVTALSPTASDAVTQMILVKAEGI EKSYSQSILLDLTDNRLQSTLKTLSFSFPEPNTVTGSERVQITAIGDVLGPSINGLASL IRMPYGCGENMINPAPNIYILDYLTKKKQLTDNLKEKALSFVRQGYQRELLYQREDG
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781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTTGGGGAAAGAAGAAAATATT 	KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI SRNVSTNVFFKOHDYIIEFFDYTTVLKPSLAFTATVKVTRADGNQLTLEERRNNVVIT VTQRNYTEYWSGSNGGNQKMEAVQKINTVPQSGTFKIEFPILEDSSELQLKAYFLGS KSSWAVHSLFKSPSKTYIOLKTRDENIKYVGSPFELVVSGNKRLKELSYMVVSRGOLVA
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541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA	FEATURES Location/Qualifiers Location (Oa) (CA) source 13535 Db /organism="Homo sapiens"
	methods of use

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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BASE CO Query Match
Best Local Similarity
Matches 3187; Conser COUNT 601 773 661 653 541 593 533 473 413 893 781 833 721 713 481 421 361 301 353 241 293 181 233 121 173 113 61 _ GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGTG GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGCACCGCCGCGCGCTG AAAGGAGACGTTAACGTTTATCCTTTATCCTTTTGGGGAAAGAAGAAAATATT ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 1107 Conservative ρ VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKV
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ERMFYGGGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDG
SFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDP
GRVIHSELQGAKSPVLTTAYITVSLLGYRKYQVFRI"

8 676 c 731 g 1021 t 74.3%; 99.9%; Score 3185.8; Pred. No. 0; 0; Mismatches 0; No. 0; DB 2 6 Indels Length 0; Gaps 600 120 840 540 592 300 240 780 832 720 772 660 712 652 480 532 420 472 360 412 180 232 172 952 892 352 292 6 0 당 S 밁 δ 망 Ś 밁 Ś 밁 Ś 밁 Ş 문 Ś 밁 Ś 밁 Ş 밁 ð 밁 \$ 밁 Ş 밁 Ś 밁 Ş 문 ð 문 Ş 밁 ঠ 吊 S 1973 1861 1913 1801 1853 1741 1793 1733 1621 1673 1561 1613 1501 1553 1441 1493 1381 1433 1321 1373 1261 1313 1201 1253 1141 1193 1081 1133 1021 1073 1013 1681 1921 961 901 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTTGAAGATGATGGG AAGTCTCCTAGTAAGACATACATCCAACTAAAAAACAAGAGATGAAAATATAAAGGTGGGA ACTCTTGAAGAAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACACAGGA GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGAGTTATACTACTGTCTTG GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAA TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTATGACAATGCAGAATAT 1980 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG GAAATTATAAGT CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA TCGCCTTTTGAGTTGGTGGTTÄGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG **AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG** GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA GATGTTCTAAAAATTCCTGTTCAGCTTGTTTTAAAAATAAGATAAAG AGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAACTG 1560 1500 2032 1972 1860 1912 1800 1852 1740 1792 1680 1620 1672 1612 1552 1440 1492 1380 1432 1372 1260 1312 1200 1140 960 1012 1320 1252 1080 1020 1072 1132

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Aichi 466-8550, Japan
Location/Qualifiers
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AY083458.1 GI:20070079
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Hashimoto, M., Ichihara, M. and
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4735 bp mRNA linear ROD 08-APR-2002
Mus musculus GPI-anchored alpha-2 macroglobulin-related protein
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                QVLEYTHER FETTOTTELLES IN ANTICK POWGSLET FILLES FROKK
KNITKS FEIRGFANTS FÜNYEMKKUMKLKPLTDVSEGS YENVOBS FEGFAEI I ATVTE
KITIS SEMASTNYFFKOHDY I IE IF DYTTULKES LINTATIVKYSK SOONQLTBEI I ATVTE
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DLYTVYDRKNNHPESORDQEMDY I QTVNYTI PQNG I I KI EF PVMSI SGELQLKAY FL
DGTSS VTVHSNFTS PSKTY I OLKTROBY I KVOS P FDLMVSGIRQFKDLSYMVI SKOQL
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KFTVKPSDKVSLR I SATQSDS LVG I VAVDKS VTLMENSNS I TMETMVHELELYNTEYY
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SLI RNPYGGCGSONMI YFA PNI Y I LDYLITKQKKOLTVNLKEKALS YMRQGVGRELLIVQRE
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3391 ACTTGGCTTAATGCACATAAGAAATTCAATGGTGAATTTTGGGAGCCAGGAAGAGTGATT 3450	3043 ACTTGGCTTAAAGGACATCAGAAATCCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATT 3102	TGTTTCCTTGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAACATAC 3	2923 AGTGCTTTTGGGAATTATGACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGA 2982	2863 TCATTTATGAGGCAAGGTTACCAGAGAGAAACTTCTCTATCAGAGGGAAGATGGCTCTTTC 2922	2803 ATTTTGGATTATCTGACTAAAAAGAAACAACTACTGACAGATAATTTGAAAGAAA	2743 ATTCGGATGCCTTATGGCTGTGGACAGAACATGATAAATTTTGCTCCAAATATTTAC 2802	2683 GTTCAGATCACTGCAATTGGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTG 2742	2623 AGTACCCTGAAAACTTTGAGTTTCCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGA 2682	2563 GGAATAGAAAAATCATATTCACAATCCTTATTAGACTTGACTGAC	503 ACAGCTCTTTCACCCACTGCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAA 	2443 GGGGCAACTGTTCTTTTTCCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTC 2502	2383 ACTTCAAGTGAAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGAT 2442	AAAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATG 2	263 CCCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTG 2 	203 CTAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTTT	GACTCCATCACTTCCTCCCCTCCCCCCCCCCCCCCCCCC	ATTTGGCTAGACACCAACATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCT	2023 ATTCATGACTTTTCTTTGGGTAGCAGTCCACATGTCCGAAAGCATTTTTCCAGAGACTTGG 2082
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TITLE
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RIausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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Villalon, D.K., Muzny, D.M., Sodergoren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                   Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Xucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
Thomas L. Casavant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 5644)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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BC052443.1 GI:30851465
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  Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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GAAAAAGGCTCTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
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                                                                                                                                                                       CACAGAGGCCATTTCAAGACTCTCGTTCTTCCGGCACTACCTCTGAGCAGTGCAGATAAG
                                                                                                                                                                                                                                                                                      GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                        AATGTGACTATTGGGGTGGATCTCCTGGAAAATAGCCCCCCACAGGTCCTTGTAAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
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                                                     ATTTATGAGCTACACATAAACGGACAATCAGAGAATGAGATCGTATTCTCCAACAGGACA 461
                                                                                                        ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC 360
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DGSFSAFGDIDSSGSTWLSAFVLRCFLEADYYIDIDDVLHRTYTWLNAHKKFNGEFW
EPGRVHHSELQGGTKSFVTLTAYIVTSYLGYKKYQPNIDVDDSTKGEBFSRGISDN
YTLAIISYALSTVGSPKAEEALNLLMQRSEKEGDTQFWLSSGPALSGSWQPRSVDIEI
AAYALLAHTLHIVSEGIPVMRWLIQQENSTGGFVSTQDTVVALKALSEFSALVHKENT
DIQLTVTGPGIPRSIHFRIDSQNLFLLHQEELHALDFITVNVSAHGSGFAICQLNVDY
NVKGSGSSKRRRSTENQEVFDLDVIVNNEDDISHLNLNVCTSHLGSERTGMVLMEVNL
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SLTGISMASTNVFFKQHDYIIEIFDYTUKRSLMFTATYKYSRSDGNQLTPBEIEN
DLYTVYTQRKNNHPESGATODEMBYIQTTYLKFSLMFTATYKYSRSDGNQLTPBEIEN
DLYTVYTQRKNHPESGATODEMBYIQTOVNYTIPQNGIIKIEPPVMSIGSGELQLKAYFL
DGTSSVTVHSMFTSPSKTYIQLKTRDEYIKVGSPFDLMVSGNRQFKDLSYMVISKGQL
VAAGKQSKRTPSLTPEASWAPKACIIAYYIAEDGEIINDILKIPQLVFENKYKLFWS
KPTVKPSDKVSLRISATQSDSLVGIVADDKSTLMENSNSITMETMVHELELYNTEYY
LGMFMNSFAVFQECGLWYLTDATLIRDSIDEVLDTEXYSERFAEENEAHIVDFEDASS
VNNVHRKNEPETWIMLDAYMGSKIYEEFETVPDSITSWVASAFVISEDLGGICTTY
DATGAFRAEFETENIATATATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSGFSASSDS1PLSETLKKVEYDNGKLNLYLDSVNESQFCVN1PTVRDYKVSN1RDGS
VSVMDYYEPRRQAVRSYNTQVKLSSCYLSPDTNCKSHTDGATDSLRRSSSLLVFCSVL
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NDTNGTIYRKTVQVPRDNGVTLVFPIKPTHLGEIPITVTAASPTASDAVTQTIVVKPE
GIEKSYSKSVLLDLTDSNVESKQQSMRFSFPPDTVIGSERVQITAIGDILGSSINGLS
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HINQGSENEIVFSNRTRLTEBSKSISVLIQTDKAFYKPKQEVKFVLTLCSDLKPYR
TSVDIFIKDDFSNVLQOWFSQKGDLGVVSKTPGLSSNPIFGDWSIQVVOXDQXYVSF
QVLEYVLPKFEVTVQTPLYCSLKSKQLNGSVIAKYTYGKPVKGSLSLTFLPLSFWGKK
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/db_xref="GI:30851466"
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/tissue_type="Brain, enriched mov
/clone_lib="NIH_BMAP_F00"
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Pred. No. 0;
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Length

5644; 90;

Gaps

164 60

240

281 180 221

341

401

1423 GAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAG 1482 	1363 GCAGTTCATAGTCTGTTTAAGTCTCCTAGTAAGACATACAT	1303 CTGGAGGATTCCAGTGAGCTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATG 1362	1243 GTTCAGAAAATAAATTATACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATC 1302 	CAGAGAAACTATACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCT	GCTGATGGCAACCAACTGACTCTTGAAGAAGAAGAAGAAATAATGTAGTCATAACAGTGACA 	GATTATACTACTGTCTTGAAGCCATCTCTCACACTTCACAGCCACTGTGAAGGTAACTCGT	TCAAGAAATGTAAGCACTAATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTT	CTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATT	AATGTAATGAATTCTTCAAATGGACTTTCTGAATACCTGGAT	ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA	AAAGGAGACGTAACGCTTACATTTTACCTTTATCCTTTTGGGGAAAGAAGAAGAAAATATT 	ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 7	661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTTGACCAGACATATTATCAATCA	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCCTACCAATA 600 	481 AAAACCTCTTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 480	
B &	D QY	Db QQ	Db QQ	Db Qy	4g 4g	d dd	D 99	D Q	Qy db	d dd	d Q	B 8	B 8	dg dy	D 5) p (S B :	о р В
2503 ACRGCTCTTTCACCCACTGCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAA 2562 	GGGGCAACTGTTCTTTTCCCATCAGGCCAACACATCTGGGAAATTCCTATCACAGTC	ACTTCAACTGAATAAATGCCACAGGCCACCAGGAGACCCTTCGGTTCCCAGTGAGGAC	AAAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAGTGGCAAATTTGATATTCTAATG	CCCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTG	2203 CTAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTT 2262	2143 GATTCTATCACTTCTTGGGTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGA 2202	2083 ATTTGGCTAGACACCAACATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCT 2142	2023 ATTCATGACTTTTCTTTGGGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGG 2082	1963 TATGACAATGCAGAATATGCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGAT 2022	1903 GAATGTGGACTCTGGGTATTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTT 1962	1843 GAACTTTATAACACAGGATATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAG 1902 	1783 AGTGTGAATCTGATGAATGCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTG 1842	TCTCTTAGGATCTCTGTGACACACACTGACTCCATAGTTGGGATTGTACCTGTTGACAAA	163 TITAAAATAGATAAAGCITATAITGGAGIJAAAGCGAAGCAGACCAICIGAGAAAGAIC 1722 	TATATTGAGAGGAGGAAATTATAAGTGATGTTCTAAAAATCCCCGTTCAGCTTGTT TATATTGCAGAGGATGGGGAAATTATAAATGATATTCTAAAAATCCCCGTTCAGCTTGTT	A CARLOL CICLI LANCACCAMMANIA LI LIMBACI COMMANDO LIGIGIANIA GIGINIA LA GALLACTRICA DE LA CARLOL CAMBRIA DE LA CARLOL CAMBRIA DE LA CARLOL CAMBRIA CONTROL CON		1533 GAGTATATAAAGGTGGGGTCACCTTTTGATTTGATGGTTAGTGGCAACAGACAATTCAAG 1592

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RESULT 12
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM Homo sapiens mRNA; cDNA AL834478 AL834478.1 GI:21740252 Homo sapiens (human) 2938 bp mRNA linear PRI 12-JUL-2002 DKFZp762L1111 (from clone DKFZp762L1111).

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 2938)

Blum, H., Bauersachs, S., Mewes, H.W., Weil, B. and Wiemann, S. Direct Submission

AL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ)762L1111) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available

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                                                                                                                                   GTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAG
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens (human)
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                             712
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ELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPY
KTSLMILIKDPKSNLTQOWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQS
FQVSEYVLPKFEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGK
KKNITKTFKLNGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGFVBILTTVTESVTGI
SRNVSTNVFFKQHDYIIEFPTYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVIT
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KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVA
VGKQNSTMFSLFENSSTPKACVIVYYIEDDGEIISDVLKIFVQUVFKNKIKLYWSKV
KAEPSEKVSLRISVTQPDSIVGIVAVUKSVNLMNASNDITMENVVHELELYNTGYYLG
MFMNSFAVFQBGGLWVLTDANLTKDYIDGVYDNLFGTQEAL"

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/clone_lib="HCHON2"
/note="cloning vector: pME18SFL3-primary culture,
chondrocytes"
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/db_xref="GI:21755237"
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/db_xref="taxon:9606"
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901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	66 ANGLAGGGCCCACCGCTCCTGACCGCCCCACCTCCTCTCCCACGGGGTTCTGCCCGGGGGGGG
RESULT 14 AX083146 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
AX083146 I300 bp DNA linear PAT 28-FEB-2001 AX083146 AX083146 AX083146.1 GI:13185055 Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Yue,H., Lal,P., Tang,Y.T., Bandman,O., Baughn,M.R., Azimzai,Y., Lu,D.A. and Yang,J. Proteases and protease inhibitors	1141 ACTCTTGAAGAAGAAGAAGAATAATGTAGTCATNACAGTGACACAGAGAAACTATNCTGAG 1200 1201 TACTGGACCGGATCTAACAGTGGAAATTAATGTAGTCAGAAAATGCAGAGAAAACTATNCTGAG 1201 1226 TACTGGACCGGATCTAACAGTGGAAATCAGAAAATGCAAAATGCAAACTGTTCAGAAAATTAATT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAATCAAGAAG 3787
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                                                                                                                                                                          CCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGA
                                                                                                                                                                                               CCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGA 4147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGAATCCCAATTATGAGGTGGCTAAGCAGCAAAGAAATAGCCTTGGGTGGTTTTGCAT 3538
                                                                  CTTCAGGCTCCCATCATCACTCTTCAGTCATTTTTTATTTTCTGTTTCAAGCTTCTGTACT 4267
                                                                                                                                  AGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAG
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/mol type="genomic DNA"
/db xref="taxon:9606"
/noTe="Incyte ID No: 3658034CB1"
239 c 289 g 419 t
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Pred. No. 1.3e-148;
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TITLE
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On Aug 1, 2001 this sequence version replaced gi:15021177.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP11-553A21 It may be shorter because we sequence overlaping sections only once, except for a 100 base everlap. The true right end of clone RP11-553A21 is at 163577 in this sequence. The true left end of clone RP11-525G3 is at 88067 is sequence. The true right end of clone RP3-397H23 is at 2000 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP11-553A21 is from the library RPCI-11.2 constructed by the of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 163577)
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AL590428 AC026605
AL590428.7 GI:15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                           285.
1166. .1384 /note="LIMC5 repeat: matches 7317. .7536 of consensus"
                                                                                                                                                                                                                434. .743
                                                                                                                                                      744. .919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                         note="AluJb repeat: matches 1.
                                                             'note="L2 repeat: matches 2626. .2708 of consensus"
                                                                                                                       note="AluJb repeat:
                                                                                                                                                                                     'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                  clone="RP11-553A21"
                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-11.2"
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                                                                                                                          matches 119.
                                                                                                                                                                                     .311 of consensus"
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/note="AluSx repeat: matches 1. .306 of consensus"
1691. 1759
                                                    note="AluY repeat: matches 1. .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                             0050. .10999
note="SVA repeat: matches 3. .
0622. .11798
note="CG island"
evidence=not_experimental
1056. .11951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSq repeat: matches 1.
3637. .13697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431. .8729 repeat: matches 1. .302 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MC3 repeat: matches 6740. .7398 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MLT2FB repeat: matches 1. .403 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluJo repeat: matches 3.
                                                                                                                          note="AluS repeat: matches 1. .63 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179. 8975
Note="MER33 repeat: matches 129. .323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1877. .8168
note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ote="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluJo repeat: matches 1.
                                                                                                                                                                                    ote="FLAM C repeat: matches 1. .123 of consensus" 451. .136\overline{3}6
                                                                                                                                                                                                                                                                                          ote="L2 repeat: matches 2588. .2707 of consensus"
561. .12844
                                                                                                                                                                                                                                                                                                                             Ote="SVA repeat: matches 519. .1386 of consensus"
038. .12152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote="MIR repeat: matches 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te="AluSq repeat: matches 1.
05. .10048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te="33 copies 2 mer tc 89% conserved"
                                                                                       e="MER39 repeat:
                                                                                                                                                                                                                                    e="AluSp repeat:
                                                                                                                                                                                                                                                                       e="AluSx repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="22 copies 2 mer tt 79% conserved"
                  e="MER39 repeat: matches 148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="AluY repeat: matches 1. .290 of consensus"
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e="LIMC5 repeat: matches 7604. .7887 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="L1MC5 repeat: matches 7536. .7604 of consensus"
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                                                                                           matches
                                                                                                                                                                                                                                    matches 2.
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                                                                                           15.
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                    .543 of consensus"
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ATTCAAACAGACAAGGCCTTATACAAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACA 456 GAGATTTTATTCTCTAATAGTACCCGCTTATCATTTGAGACCAAGAGAATATCTGTCTTC GAGATTTTATTCTCTAATAGTACCCGCTTATCATTTGAGACCAAGAGAATATCTGTCTTC

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Matches 232;
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                   Local Similarity
                                                                    /note="L1M4 repeat: matches 4499. .4833 of consensus"
27866. .27943
/note="MLT1J repeat: matches 410. .492 of consensus"
                                                                                                                                                                          note="FLAM_C
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'note="Alusx r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LTR29 repeat: matches 571.
|4832. .15863
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                                                                                                                                                                                                                                                                                                                                                                                        note="AluSx repeat: matches 142. .309 of consensus"
1243. .24416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSg/x repeat: matches 87. .262 of consensus"
?895. .23001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="LIMA10 repeat: matches 5026. .6320 of consensus"
                                                                                                                                               ote="AluJb repeat: matches 7. .311 of consensus"
                                                                                                                                                                                                                                                                             ote="MLT1A1
179. .25484
                                                                                                                                                                                                                                                                                                                                 ote="AluSx repeat:
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Lote="Alusx repeat: matches 62. .142 of consensus"
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lote="THE1B repeat: matches 1. .364 of consensus"

.480. .21775

lote="Alusg repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ote="AluJo/FRAM repeat: matches 179. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="AluSg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote="FLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ote="Alusg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote="L1M3c repeat: matches 734. .820 of consensus"
5.4%; Score 232; DB 9;
100.0%; Pred. No. 6.9e-40;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                      te="AluSx repeat: matches 1. .299 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="AluSq/x repeat: matches 12. .112 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="AluSg repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e="L2 repeat: matches 2208. .2414 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="16 copies 2 mer ac 96% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="L2 repeat: matches 2636. .2734 of
                                                                                                                                                                                                                       copies 2 mer at 100% conserved"
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                                                                                                                                                                                 C repeat: matches 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat:
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                                                                                                                                                                                                                                                                                              repeat: matches 1. .363 of consensus"
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Search completed: January 16, 2004, 18:48:41 Job time : 15013 secs	80730 CTCTTCTCAGATTTTAAGCCTTTACAAAACCTCTTTAAACATTCTCATTAAGG 80781	457 CTCTTCTCAGATTTTAAGCCTTTACAAAACCTCTTTTAAACATTCTCATTAAGG 508	80670 ATTCAAACAGACAAGGCCTTATACAAGCCAAAGCAGAGTGTAAGTTTCGCATTGTTACA 80729

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Human platelet all
Hydrophobic domain
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Human CD109 K15 ya
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24-APR-2001; 2001US-285713P
14-FEB-2002; 2002US-356163P
                                                                                                                                                                                                                                                       Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                   Human r150 gene #1.
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                                        24-APR-2002; 2002WO-CA00560
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26..4312
                                                                                                                        /product= "Human r1520 protein #1"
/transl_except= (pos:2132..2134, aa:Xaa)
/note= "Xaa corresponds to Ser, Tyr"
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DNA encoding human Human cDNA SEQ ID Human polynucleoti

Human alpha-2-macr Human pregnancy zo Human platelet all

Gene #3730 used to DNA encoding novel Human ORFX ORF39 p

DNA encoding novel

Database

Title: Perfect score:

OM nucleic -

92

Searched:

Human gene express
Bovine EST associa
Human gene express
C. elegans alpha-2
C. elegans alpha-2
Drosophila melanog
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Scoring table: Sequence:

Result No.

Score

4281.2 4224.4 4224.4 4223.4 4223.4 4222.8 4222.8 4222.8

SXCCCCCCCCCX BX PPPPX BRX PXX

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Query Match
Best Local Similarity
Matches 4283; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidy inositol (GP)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is a gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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                                                                                                           New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombine thrombocytopenia, autoimmune diseases, or organ or bone marrow
                                                                                                                                                                                                        WPI; 2002-713450/77.
P-PSDB; ABB82165.
                                              Claim 1; Fig 1a; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 K1; gene; ss.
    The invention relates to isolated nucleic acid molecules encoding CD109
                                                                                                                                                                                                                                                                            Schuh A,
                                                                                                                                                                                                                                                                                                                        (SCHU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC polypeptides. These nucleic acid molecules include the human cDNA CS sequences comprising CD109 K1, CD109 K1-7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioseter-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC contracting or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the coagulation or fibrinolytic systems, cativative abnormalities CC activation, increased or impaired platelet aggregation and CC fibrinolytic systems, or impaired platelet aggregation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC contraction, thrombosis, embolism, peripheral vascular disease, myocardial infarction, thrombosystemia, autoimmune diseases, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for CC treating these conditions. The present sequence represents the human contracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 4286;
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Best Local
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  GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT
                                                                                               TCACAACAAAGTGATCTTGGAGTCATTTCCCAAAACTTTTCAGCTATCTTCCCATCCAATA
                                                                                                                                                                                                                                                                              AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG
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                                                                                                                                                              TCACAACAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA
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660 712 540 592 480 532 420 472 360 412 300 352 240 292 51; Gaps

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2933 AAAAAGAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2992	GTTGACAAAGTGTGAATCTGATGAAT 1800	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 	용 성
873	1740	1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG	B 8
813	1680 1792	1621 GARATTATAAGTGATGTTCTAARAATTCCTGTTCAGCTTGTTTTTAARAATARGATARAG 	음 성
ACTITICTCATTICCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT	1620 1732	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG	8 8
SBI TCACARICCATCLTATAGACTIGACTAGACATAGGCTACAGAGTACCCTGAAAACTTIG	1560 1672	1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA	음 성
21 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAATCATAT	1500	1441 TCCCCTTTTGAGTTGGTCGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA	용 성
CCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGGTCACAGCTCTTTCACCCACT	1440	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 	B &
401 GCCACAGGCCACCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTT 513 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT	1380	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT	음 <i>청</i>
341 AGGIPAGICATIGAGAAAAGIGACAAATITGATATTCTAATGACITCAAGIGAAATAAAT 453 AAGGIPAATCATTGAGAAAAGTGACAAATITGATATTCTAATGACTTCAAATGAAATAAAT 453 AAGGIPAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAATGAAATAAAT	CAGTGAG 1320	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTC	음 성
BI GGIGANGAAITIGCITIGGAAAIAACTATATTCAATAATTGAAAGAIGCCACTGAGGIT	1260	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	B 8
GAGCTCCAAGCCTTCCAACCATTTTCATTTTTTGAATCTCCTACTCGTTATCAGA	1200	1141 ACTCTTGAAGAAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG	B. 8
GIGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG	1140	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCGACCTG	음 성
A TIGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTTGG	1080	1021 AATGIGTTCTICAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG	B 8
GGIAGCAGICCACAIGTCCCGAAAGCATTTTCCAGAGACTTTGGCTAGACACCAAC	1020	961 GTAGAAATTTTAACCACAGTGACAGAATCAGGTTACAGGTATTTCAAGAAATGTAAGCACT	음 장
GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG	960	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	B &
921 IISKASAISCAAKUTIKKISAISSAITAIRIITIGAISJIETITAISACAAISCASAATAT 	900	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAAA	B 8
861 TATTATTIAGGCATGTTCATGAATTCTTTTGCAGTCTTCAGGAATGTGGACTCTGGGTA 973 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA	952	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAAATATT	음 왕
913 GCCTCTATIGATATTACAATGGAAAATGTIGGTCCATGAGTTGGAACTTTATAACACACAGA	780	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG	B 8
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AAD49440 standard; DNA; 5882 ₽P

24-MAR-2003 (first

Human blood cell surface antigen, CD109 encoding DNA #2

Human; GPI-anchored TGF-betal binding protein; r15(glycosylphosphatidyl inositol; transforming growth therapy; blood cell syrface antigen; CD109; ds. factor-betal; cancer;

sapiens.

WO200285942-A2

24-APR-2002; 2002WO-CA00560

24-APR-2001; 2001US-285713P. 14-FEB-2002; 2002US-356163P.

(UYMC-) UNIV MCGILL.

Philip Þ Tam ₽,

WPI; 2003-093100/08

Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for treating cancer

Disclosure; Fig 17; 127pp; English.

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability

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      The invention relates to isolated nucleic acid molecules encoding CD109
C polypeptides. These nucleic acid molecules include the human cDNA
C sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants.
CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5
CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5
CC family of thioester-containing proteins. The CD109 polypeptides can be
expressed by standard recombinant methodology. The CD109 nucleic acid,
CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
CC for treating or detecting a disease or disorder, e.g. conditions
CC associated with endothelial activation, platelet activation, activation
CC of the complement system, quantitative or qualitative abnormalities
CC and of the complement system, quantitative or qualitative abnormalities
CC of platelet function, increased or impaired attalet aggregation and/or
CC fibrinolytic systems, or impaired activation of the coagulation and/or
CC fibrinolytic systems, or impaired activation fithe coagulation. These
CC are also useful for treating cardiovascular disorders, stroke, myocardial
CC infarction, thrombostis, embolism, peripheral vascular disease, organia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD109; alpha2 macroglobulin; thioester; cerebroprotective; c: immunosuppressive; haemostatic; anticoagulant; thrombolytic; cardiovascular; vasotropic; gene therapy; CD109 KI-H7; gene;
                                                                                                                                                                                                                                                                                                                          New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
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CTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT
                                                            ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG
                                                                                                                  GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC
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Gaps

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Score 4223.4; Pred. No. 0;

DB 2 25; Sequence

5883 BP;

1696 A; 1173 C;

1241 G;

1772 T; 1 other;

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                                                    The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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P-PSDB; AAE32013.
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14-FEB-2002;
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/transl_except= (pos:2219..2221, aa:/note= "Xaa corresponds to Ser, Tyr"
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Oy 1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG	TATTI TATTI	OY 1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCCTCTTG 1740	Qy 1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTATATATA	1441 TCG 1553 TCG 1501 GTA: 	1321 1433 1381 1493	Qy 1201 TACTGGAGCGGATCTAACAGTGGAAAATGAAAATGAAAATAATTAT	Qy 1081 AAGCCATCTCTAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCTACTG

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                                                                                                                                  The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its minetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the complement system, quantitative or qualitative abnormalities CC and of the complement system, quantitative or qualitative abnormalities CC in the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC infarction, increased or impaired activation of the coagulation and/or CC crossplantation, thrombosis, embolism, peripheral vascular disease, myocardial CC infarction, thrombosis, embolism, peripheral vascular disease, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids CC or their antisense nucleotide sequence are useful in gene therapy for CC transplantation, or bone marrow transplantation. The CD109 nucleic acids CC D109 K1 variant cDNA sequence.
Query Match
Best Local Similarity
Matches 4285; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombosytopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                  Sequence 4761 BP;
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BI AAGTATCAGCCTAACATGATGTGCAAGAGTCTATCCATTTTTGGAGTCTGAATTCAGT	B &	2101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2160	유 성
GCCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCCTGGGATATAGA 	dg dy	2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTTGGCTAGACACCAAC 2100 	유 성
CAGAMATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATGATAGTGAGCTTCAAGGT 	b &	1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 2040 	음 성
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2821 AAAAAGAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880	Qy Db	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800 	음 성
TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT	B &	1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1740 	음 성
GAGANGTTCTTGGTCCTTCATCATGGCTTAGCCTTATGGCTTATGGC	S & &	1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTAAAAATAAGATAAAG 1680 	유
AGTITICTCATITICCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT	å å	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGG 1620 	유
B1 TCACAST CLATCTIATIAGACTIGACCIGACANTAGGCIACAGGAGTACCCTIGAAAACTITIG	g dg	1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560 	유
21 GCTICTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAATCATAT 21 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 33 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAAATCATAT	}	1441 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 1500 	유 성
61 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACCACTGTTTCACCCACT 	o og	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGGTGGAAAATATAAAGGTGGGA 1440 	유 성
01 GCCACAGGCCACCAGCAGCCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 13 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 13 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT) P &	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380 	유왕
AGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAATTAAATTAATT	d dd	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320	유 성
GGTGANGANITIGCITIGGANATANCTANNITICANTANITIGANGANGCIGCGACHGNGGIT	D	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	유
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ATGGAACTTTGGCTGTGA
                                                                                                                                                                       CTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT
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                                                         TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTTCTGTACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 K1-H7; variant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2b;
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/product= "CD109 K1-H7
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The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1. CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alphaz macroglobulin (alphazM)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities CC and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired activation of the coagulation and cC of contraction, increased or impaired or increased immune activation. These CC of contraction activation or impaired activation of the coagulation and/or CC contraction, thrombosis, embolism, peripheral vascular disease, cCC thrombocytopenia, thrombocythemia, autoimmune diseases, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids cor their antisense nucleotide sequence are useful in gene therapy for CC creating these conditions. The present sequence represents the human CC CD109 K1-H7 variant CDNA sequence.

BP; 1708 A; 1174 C; 1241 G; 1772 T; 0 other

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Query Match
Best Local Similarity
Matches 4285; Conserv
  Conservative
          98.5%;
 0,
         Score 4222.8;
Pred. No. 0;
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2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG	2101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG	2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTTGGATTTTGGCTAGACACCAAC	1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG	1921 TTGACAGATCCAAACCTCACGAAGATTATTATTGATGGTGTTTTATGACAATCCAGAATAT 1980	73 1	୍ଦ୍୍	A A	0 - 0	33 — ნ წ—ნ	61 Q 73 Q	1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560 	53 T	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440 	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG	н-н	1141 ACTCTTGAAGAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC

221 GCCTCCAACCCTTCCAACCATTTTTCAATTCTTCATTTTCAACCTACTA
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Matches 4283;
                                                                                                                                                                                                                                    The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or meonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova coding sequence.
                                                                                                                                                                                                        Sequence 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune
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Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells.

Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport;

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
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P-PSDB;
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16-MAR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
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  autoimmune disease;
                                                      Human; secreted protein;
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                                                                              domain protein cDNA HP02837 isolated from HT-1080 cells.
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                                          n; membrane protein; hydrophobic domain; differentiation induction; material transport;
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98JP-0364315.
99JP-0069811.
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Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -

Claim 3; Page 244-246; 410pp; English.

CC differentiation induction, the material transport and the biophylaxis of CC cells. Membrane proteins have important roles as signal receptors, ion CC channels and transporters. The present sequence is the coding sequence CC protein encoded by the present sequence may be a secretory or a membrane CC protein. The encoded protein activity, immune stimulating or suppressing CC activity, haematopoiesis activity, tissue growth activity, haemostatic CC activin/inhibin activity, anti-inflammatory activity and tumour CC inhibition activity, anti-inflammatory activity and tumour CC inhibition activity, anti-inflammatory activity and tumour continuing cactivity and seems sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's CC disease, and cancer via gene therapy.

4335 BP; 1295 A; 838 C; 922 G; 1280 T; 0 other;

AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG ATGCAGGGCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCGCTG GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGA Score 4216.6; Pred. No. 0; 0; Mismatches <u>.</u> 멂 4 21; Length Indels 51; 4335 Gaps 300 360 300 240 240 180 180 120 120 60 60

2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT		aagtctcctagtaagacatacatccaactaaaaacaagagatgaaaatataaaggtggga	٠₹
2401 GCCACAGCCACCAGCAGCCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT	QY Db	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTTGTTT 1380 	ਰ ਵ
	d dd Ao	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320	ט ע
	γ dα γ	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	ъ ч
	Ωy	1141 ACTCTTGAAGAAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200 	σ <
	da Ao	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	σ <
	40 40	1021 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG 1080	σ ≺
	D 69	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020 	σ <
	dg dy	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	σ <
	- P &	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 	8 4
	Db Qy	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTTGGGGAAAGAAGAAAAATATT 840 	ъ ч
	o du	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780 	σ '
1741 KCACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTCACAAAAGTGTGAATCTGATCAAT	90 80	661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720	р Ч
	- B 8	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGACGAGACATATTATCAATCA	σ <
	Db Q	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600 	ъ 4
	S B S	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540 	₽ ₹
) D (V	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 480 	ਰ ਵ
	}	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	ਰ ਵ
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                                       Human; GPI-anchored TGF-betal binding protein; r150 protein; can glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; blood cell syrface antigen; CD109; gene; ds.
                                                                Human
                                                                            24-MAR-2003
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GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTT
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                                                               cell surface antigen, CD109 encoding DNA
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Location/Qualifiers
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/*tag= a
/product= "Human CD109
                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                                                                               Matches 4142;
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inosicol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 109-112; 127pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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14-FEB-2002;
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    ACCTCTTTAAACATTCTCATTAAGGACCCCCAAATCAAATTTGATCCAACAGTGGTTGTCA
                                                                         TTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAG
                                                                                                                       TATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACCCGC
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/note= "Xaa corresponds to Ser, Tyr; No start
and stop codon"
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                                    GAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACTAAT
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P-PSDB; AAE32015.
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/tranel_except= (pos:2044..2046, aa:)
/note= "Xaa corresponds to Ser, Tyr;
and stop codon"
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Best Local Similarity
Matches 4144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein according two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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                                    AATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTGAAA
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                        TATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTT
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CC The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the complement system, quantitative or qualitative abnormalities CC and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired activation of the coagulation or fibral activation of the coagulation and or CC of platelet systems, or impaired activation of the coagulation and/or CC controlytic systems, or impaired activation of the coagulation and/or CC activation, increased or impaired activation activation. These cc are also useful for treating cardiovascular disorders, stroke, myocardial cc infarction, thrombosis, embolism, peripheral vascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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                                                                                                                                               TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTTGGGAATTAT 2940
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The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 cf family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful cor treating or detecting a disease or disorder, e.g. conditions cassociated with endothelial activation, platelet activation, activation of the complement system, quantitative or qualitative abnormalities and of the complement system, quantitative or qualitative abnormalities can of platelet function, increased or impaired platelet aggregation and confidency increased or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired or increased immune activation. These care also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolsism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nuc or their antisense nucleotide sequence are useful in gene them nucleic acids

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T 3120	3061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGGTTCAAGGT
T 3060 T 3172	3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT
T 3000 T 3112	2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTTTAAGATGTTTCCTTGAAGCCGAT
T 2940 T 3052	2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTTGGGAATTAT
T 2880	2821 AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT
T 2820 T 2932	2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT
C 2760	2701 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGG
T 2700 T 2812	2641 AGTTICTCATITICCTCCTAATACAGIGACTGGCAGIGAAAGAGTTCAGATCACTGCAATT
G 2640 G 2752	2581 TCACAATCCATCTTATTAGACTTGACAATAGGCTACAGAGTACCCTGAAAACTTTG
T 2580 T 2692	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT
T 2520	2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT
T 2460 T 2572	2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGGCAACTGTTCTTTTT
T 2400 T 2512	2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT
T 2340 T 2452	2281 GGTGAAGAATTIGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTT
A 2280 A 2392	2221 GAGCTCCAAGCCTTCCAACCATTTTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGA
G 2220 2332	2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTACAACTACTCCAGTG
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Db 3233 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCCTGGGATATAGA 3292

Qy 3181 AAGTATCAG 3189
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Db 3293 AAGTATCAG 3301

Search completed: January 16, 2004, 14:38:44 Job time: 1046 secs

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lifiers		<pre>1 binding protein; r15 1; transforming growth</pre>		•		BP.		ALIGNMENTS	ABA06869	ABX70464	AAL49817	ABS59327 ABO93897	ABK92035	AAC74484	ABN97232	ABL12152 AAS92193	ABL20610	ABL19705 ABL19704	ABL12153	AAC90952 ABL20611	AAC90951	ABX47702	AAZ13539	AAZ15521 AAS70864	ABX08843	AAF81735 AAX20449	ABV77330	ABA08825	ABQ79969	96	AAD49437	AAA60199	201	AAL49816
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		protein; cancer; factor-betal;							Human cDNA SEQ ID Human polynucleoti	acoding hu	Human platelet all	alpha-2-n	DNA encoding novel		Gene #3730 used to	Drosophila melanog			Drosophila melanog	elegans reorbila	C. elegans alpha-2	EST	Human gene express	Human gene express	w	Human protease and	-1 protei	Human polynucleoti		CD109 K15	Human r150 DNA #2.	Hydrophobic domain	- 1	Human platelet all

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601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAGTCTATTCAG
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Best Local Similarity
Matches 4283; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GFI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is a gene encoding human r150 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 91-93; 127pp; English.
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    New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
transplantation
                                                            WPI; 2002-713450/77.
P-PSDB; ABB82165.
                                                             P-PSDB;
                                                                                                 Schuh A,
                                                                                                                                                               07-MAR-2001; 2001US-273814P
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                                                                                                                                                                                                                                                                                                                                                                   CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human;
                                                                                                                                                                                                                                                                                                                                                                                                            Human CD109 K1 protein encoding cDNA.
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of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired activation of the coagulation and/or ribrinolytic systems, or impaired activation of the coagulation and/or are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, by comparing thrombocythemia, autoimmune disease, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human CD109 KI cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation
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Sequence 4761 BP; 1420 A; 912 C; 1016 G; 1413 T; 0 other;

밁 S 밁 Ś 밁 S 밁 S 밁 á 밁 5 밁 ð 밁 S 밁 Ś 밁 S Ś 밁 Matches 4286; Query Match Best Local Similarity 199 601 653 541 593 481 533 421 473 361 413 301 353 293 181 233 121 173 241 113 61 -GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGGCCCACCTCTGCGTGTGCACCGCCGCGCTG AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATTACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG **AAGCCAAAGCAAGTGAAGTTTCGCATTGTTACACTCTTC** ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA ATGCAGGGCCCACCGCTCTGACCGCCGCCCACCTCTCTGCGTGCACCGCCGCGCGCTG Conservative 98.5%; 0 Score 4224.4; Pred. No. 0; Mismatches DB 24; Length 1; Indels CAGATTTTAAGCCTTAC 51; Gaps 540 720 772 660 712 600 652 592 480 532 420 472 360 412 300 352 240 292 180 232 120 172 60

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Claim 1; Fig 1a; 156pp; English

invention

to isolated nucleic acid molecules encoding CD109

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Result No.

Match

Length

DB

AX534934 IJ

AX534934 Sequence AF410459 Homo sapi

Description

4224.4 4224.4

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Listing first 45 summaries
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Pred. No.

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number of results predicted by chance to have a VERSION KEYWORDS RESULT 1
AX534934
LOCUS
DEFINITION
ACCESSION REFERENCE 0 0 0 0 0 0 a G AUTHORS TITLE a ORGANISM JOURNAL 2448. 1969. 730. 2709 2709 3185. 155. 154. 171.6 167.6 182 177.4 175 232 230 219.6 203.8 Schuh, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides and methods of use Patent: WO 02070696-A 1 12-SEP-2002; Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Homo sapiens Homo sapiens (human) AX534934.1 GI:25261474 Sequence 1 from Patent WO02070696. AX534934 4.2 251250 4.1 91419 .4 176144 4 163577 4950 122013 164414 191258 149597 176144 144589 168503 2629 4715 4527 4560 4579 4335 4335 3535 3535 4761 5895 RATA113A DME269538 RNA113 AC012408 XELENDO AC092399 AC092395 AC115484 AE003649 AC112668 AC118254 GGOVOM AY122084 BC036299 BC051037 DME269539 AY118302 DROSADHOB AC034271 CIN431688 AX083146 AX534942 AX537612 RATA113 GPIMSPB 4761 bp ALIGNMENTS Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. DNA

L63543 Xenopus lae AC092399 Drosophil

D84339 Cavia porce J03524 Rat alpha-1 J03552 Rat plasma AJ269538 Drosophil AC012408 Homo

AC092395 Drosophil AC115484 Drosophil

AE003414 Drosophil AC118254 Mus muscu

Drosophil

AX054953 Sequence
AX054954 Sequence
AX118302 Drosophil
X78801 G.gallus mR
AY122084 Drosophil
AJ26939 Drosophil
AC112668 Mus muscu
AC112684 Mus muscu
AC112684 Rat mRNA fo

AL834478 Homo sapi AK095888 Homo sapi AX083146 Sequence AL590428 Human DNA AC012408 Homo sapi AJ431688 Ciona int D83196 Limulus sp. AC097023 Rattus no AL591480 Human DNA AC034271 Homo sapi

AX534942 Sequence AX534944 Sequence AX537610 Sequence AX537612 Sequence

AY083458 Mus muscu BC052443 Mus muscu

AX534940 Sequence AX534938 Sequence AX534936 Sequence

linear

PAT 22-NOV-2002

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                                                                                                                                                                                                                                                                                                                      5883 bp
Homo sapiens CD109 (CD109) mRNA,
AF410459
AF410459.1 GI:19071208
                                                                                                                                                         Lin,M., Sutherland,D.R., Horsfall,W., Totty,N., Yeo,E., Nayar,R. Wu,X.F. and Schuh,A.C.
Cell surface antigen CD109 is a novel member of the alpha(2)
macroglobulin/C3, C4, C5 family of thioester-containing proteins
Blood 99 (5), 1683-1691 (2002)
                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5883)
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Lin,M., Sutherland,D.R.,
Wu,X.-F. and Schuh,A.C.
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Submitted (14-AUG-2001) Medicine,
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                            College Circle, Room 7366, To
Location/Qualifiers
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organism="Homo sapiens"
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       ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC
                                       GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
                                                         GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
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Query Match
Best Local Similarity
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                                                                                  AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
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ANTGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
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4748
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VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKV
KAEPSEKVSLRISVTQPDSI'GIVAVDKSVNLMVASNDITMENVVHELELYNTGYYLG
MFMNSBAVFQECGLWVLTDANLTKDYIDGVYDNAEYAEFMEENEGHIVDIHDFSUS
SSHVRKHFPETWIMLDTNMGYRIYQBEFEVTVPDSITSWVATGFVISEDLGLGLTTTPV
ELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSNE
INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTASDAVYQMILVXAEGI
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gvellehcpsqvtvkaellktasnltvsvleaegvfekgsfktitlpslplusadeiy
elrvtgrtodeilfsnstrlsfetkrisvfigtdkalykpkoevkfrivtlfsdfkpy
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/db_xref="taxon:9606"
/clone="K1"
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IRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQREILYQREDG
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FQVSBYVLPKFEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGK
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/note="associated with the Gov alloantigen system"
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LALITYALSSVGSPKAKEALNMLTWRAEQEGGMCFWVSSESKLSDSWQPRSLDIEVAA
YALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTODTTVALKALSEFAALMNTERTN
IQVTVTGPSSPSPVKFLIDTHNRLLLQTAELAVVQPMAVNISANGFGFAICQLNVVYN
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LSGFMVPSEAISLSETVKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTODAS
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2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 2520	Db Qy	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440
2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 2460 	B 29	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAGAAGTAGCATGGCAGTTCATAGTCTGTTT 1380
2341 AAGGTAATCAITGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	D 09	1261 ACTGTCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320
2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGAAKGATGCCACTGAGGTT 2340 	B 8	1201 TACTGCAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT
2221 GAGCTCCAAGCCTTCCAACCÂITTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA 2280 	₽ <i>Q</i>	
2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTTGGACTACTACTACTACTCCAGTG 2220 	₿ <i>&</i>	
2101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2160 	B 8	1021 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG 1080
2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 2100	B &	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020
1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 2040 	B 8	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT
1921 TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTTATGACAATGCAGAATAT 1980 	B &	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 953 ACAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGAAGAGAGAG
1861 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 	පි රි	781 AAAGGAGACGTAACGCTTACATTITTACCTTTATCCTTTTTGGGGAAAGAAAGAAAAATATT 840
	B &	721 ATGAATICTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780
1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800 	ρ δ δ	661 GITTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720
1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1740 	용 <i>성</i>	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA
1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 1680 	D Q	541 TCACAACAAAGTGÀTCTTGGAGTCATFTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600
1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620 	Db Qy	481 AAAACCICITTAAACAITCTCAITAAGGACCCCAAATCAAAT
1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560 	Db .	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 480
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CTGAATTTG	CTGTGGCTTTAAAGGCTCTGTCTGAATTTG	SHEEL GOAATCCCCAATTATGAGGTGGCTAAGCAGGCAAAGAATAGC	OY 3421 GATATTGAAGTTGCAGCCTATGCACTGCTCTACACTTCTTACAATTTCAGACTT	Qy 3361 ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGG	Qy 3301 AGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGAACAACAAGAAGGTGG	Oy 3241 AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCA	Qy 3181 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTG	Qy 3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTC	Oy 3061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGGTTCAAGGT	Qy 3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACT	Qy 2941 GACCCTTCTGGGAGCACTTGGTTGTCTTTGTTTTTAAGATGTTTCC 	Qy 2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTG	Qy 2821 AAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT	Qy 2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATC'	Qy 2701 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTV	Qy 2641 AGTITICTCATITICCTGCTAATACAGTGACTGGAAGGGTAAAGAGTTCAGATCACTGCAAT	QY 2581 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTT	Db 2633 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAAGGCTGAAGGAATAGAAAAATCATAT	Oy 2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGA
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/organism="womo sapiens" /mol_type="genomic DNA"	Location/Qualifiers	Schuh, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides and methods of use patent: WO 02070696-A 5 12-SEP-2002;	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX534938 AX534938.1 GI:25261482 Homo sapiens (human)	5895 bp DNA Trom Patent WOO2070696.												CTGATTGACACACACAACGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA 3832 ATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTGCTATTTGTCAGCTCAATGTTGTA 3729		GARAGGACARATATCCARGTGACCGTGACGGGGCCTRGCTCRCCARGTCCT 3651

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QY 1021 AARGTGTTCTICAACCAACATGTTACATCAGTTTTTTTGATTATACTACTGTCTTTG 1080 Db 1021 AARGTGTTCTTCAAGCAACATGATTACATCAGTTTTTTTGATTATACTACTGTCTTTG 1140 QY 1081 AAGCCATCTCCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	901 ANTGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	ANAGGAGACGTBACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAAAATATT 8	Oy	81 41	421 421 421	301 301 361	121 181 181 241	1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG 60 1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG 60 1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCCTCTGCGTGTGCACCGCCGGAGGA 120 61 GCCGTGGCTCCCGGGCCTCCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA 120 1)95-3.rge

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Best Local Similarity 98.8%;
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181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 240

AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA

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Score 4219.8; Pred. No. 0; 0; Mismatches

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Sequence 3 from Patent WO02070738.
AX537612
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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VTORNYTEYNGGSNIGGNOKMEAVOKLNYTVOKOGTFKLEFF LILEDSSELOLKAYELGS
KSSMAVHSLFKS PSKITI JOLKTRDEN I KVOGS PFELVVSGNKRLKELSYMVVSRGQLVA
VGKQNSTMFSLITENSNTFKACVI VYY I EDDGEI I SDVLKI PVOLVFKUKI KLYNGKV
KAEPBERKVSLRI SVTQDDS I VGI VAVDKSVNLANASNOI TMENVVHELELYNTGYYLG
MFMNS FAVFQECGLWULTDANLIKDY I DOVINEAYARF MEENEGH I VDI HDFSLGS
SPHVRHEPETWI HLDTNMGSRI YQEFEVTUPDS I TSWVATGFVI SEDLGLELTTTPV
ELQAFQPF I FLNLPYSVI RGEEFAL EI TI FNYLKDATEVKVI I EKSDKFD I LMTSNE
INATGHQOTILL VPSEDGATVLFP IR PTHILGEI F I TVTALSPTASDA VTQNILVKAEGI
EKSYSQSILLDLTDNRLQSTLKTLSFS FPENTTVGSERVQI TA IGDVLGFS INGLASL
IRMPYGCGEQNNI INFARNI Y ILDYLTKKKQLTDNIKEKALSFMGQGYQRELLYQREDG
SFSAFGNYDBGGSTMLSAFVLRCFLBADPY ID LOQNULHETYTMLKGHOKSNGEFNDP
GRVIHSELQGGNKS PVILTAY I VTSLLGYRKYQPM ID VQES I HFLESEF SRGI SDNT
LALITYALSSYGS PKAKEALMULTWRARDEGGHOFWVSSESKLDSSOQPRELID EVAA
YALLSHFLQFQTSEGI PIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTN
IQVTVTGFSSJSS PKELI DTHRRLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTN
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KTSLNILIKDPKSNLIQQWLSQOSDLGVISKTFQLSHFILGDKSUQVQVNDQTYYQS
FQVSEXYLLPKEVTLQFLYCSMNSKHLNGTITAKYTYKPKFVKGDVTLTFLPLSFKPK
KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI
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GVELLEHCPSQVTVKAELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY
                                    VSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFIFCFK
LLYFMELWL"
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/db_xref="taxon:9606"
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/mol type="genomic DNA"
                                                                                                                                                VKASGSSRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNL
LSGFMVPSEAISLSETVKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDAS
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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11379.047 Million cell updates/sec
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Human r150 gene #1
Human CD109 K1 pro
Human D100d cell s
Human D109 K1-H7
Human r150 DNA #1.
Human CD109 K1 var
Human CD109 K1-H7
Human CD109 K1-H7
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AAD49434
Standard; DNA; 4369
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ABL12152
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Human gene express
C. elegans alpha-2
C. elegans alpha-2
Drosophila melanog
Drosophila melanog
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Human secreted pro
Alpha-1 proteinase
Human protease and
Human secreted pro
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Hydrophobic domain
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Human blood cell s
Human r150 DNA #2.
Human CD109 K15 pr
Human CD109 K15 va
DNA encoding human
Human cDNA SEQ ID
Human polynucleoti
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Angiogenesis-assoc
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                     human
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ALIGNMENTS

AAD49434;

24-MAR-2003 (first entry)

Human r150 gene #1.

Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.

Homo sapiens.

26..4312

ocation/Qualifiers

WO200285942-A2

24-APR-2001; 2001US-285713P. 14-PEB-2002; 2002US-356163P. 24-APR-2002; 2002WO-CA00560

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ID ABQ79964 standard; cDNA; 4761 BP.

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AC ABQ79964;
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DT 23-DEC-2002 (first entry)
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DE Human CD109 K1 protein encoding cDN.
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CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 (amily of thioseter-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired platelet aggregation and CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation. These CC are also useful for treating cardiovascular disorders, stroke, myocardial cinfarction, thrombosis, embolism, peripheral vascular disease, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for CC CD109 K1 CDNA sequence.
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Sequence 4761 BP; 1420 A; 912 C; 1016 G; 1413 T; 0 other;

밁 ঠ 밁 8 밁 Ś 밁 S ঠ 문 밁 Ş 밁 ð 밁 Ś 문 ક S 밁 밁 Query Match Best Local Similarity Matches 4286; Conserv 661 109 653 541 593 481 421 473 361 413 301 353 241 293 181 233 121 173 113 61 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTTACCTCTGAACAGTGCAGATGAG ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTGCGTGTGCACCGCCGCGCTG **AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGTGAAGTTTCGCATTGTTACACTCTT** ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA 120 **AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG** Conservative 98.5%; 0; Mismatches Score 4224.4; Pred. No. 0; DB 24; Length 4761; 1; Indels CAGATTTTAAGCCTTAC 51; Gaps 660 720 652 540 592 480 532 420 360 300 240 180 232 172 60 472 412 352 292

Claim 1; Fig la; 156pp; English.

The invention relates to isolated nucleic acid molecules encoding CD109

transplantation

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Database :
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SUMMARIES

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AOTHORS TITLE JOURNAL	REFERENCE	KEYWORDS SOURCE ORGANISM	DEFINITION ACCESSION VERSION	AX534934
Schun, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides and methods of use Patent: WO 02070696-A 1 12-SEP-2002;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	 Homo sapiens (human) Homo sapiens	Sequence 1 from Patent WO02070696. AX534934 AX534934.1 GI:25261474	

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Homo sapiens CD109 (CD109) mRNA,
AF410459
AF410459.1 GI:19071208
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Wu,X.F. and Schuh, A.C.
Cell surface antigen CD109 is a novel member of the alpha(2)
macroglobulin/C3, C4, C5 family of thioester-containing proteins
Blood 99 (5), 1683-1691 (2002)
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                                         Direct Submission
Submitted (14-AUG-2001) Medicine, U
College Circle, Room 7366, Toronto,
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2513 GCCACAGGCCAGCAGACCCTÜCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTT 2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT	B & B		1433 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1492 1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440
04229	\$ &		CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTTGTTT
2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	B 8		
2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTGAATGATGCCACTGAGGTT 	90 V2	N O	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT
2221 GAGCTCCAAGCCTTCCAACCÂTTTTTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGA	B &	ν ο	1141 ACTCTTGAAGAAAGAAGAAGTAATGATGATAACAGTGACACAGGAGAAACTATACTGAG 1200
2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG	₽ <i>&</i>	ν ο	1081 AAGCCATCTCTAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC
2101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG	B &	N O	1021 AAIGTGTICTTCAAGCAACATGAITACATCATTGAGTTTTTTGAITATGATGACTACTGTCTTG 1080
2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTTGGATTTTGGCTAGACACCAAC	B &	ν ο	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020
1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG	B 9	N	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT
1921 TIGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTATGACAATGCAGAATAT	B 8	N	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAA 900
1861 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTQGACTCTGGGTA 	B &		781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTTGGGGAAAGAAGAAGAAAATATT 840
1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTTGGAACTTTATAACACAGGA 	p &		721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780
1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT	B 8		661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720
1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAAGGATCTCTGTG	B 8		601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGACCAGACATATTATCAATCA
1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 	B 5		541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600
1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGAGG	<u> </u>	~ 5	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540
1501 GTATCCAGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTTAACA 	B &		421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 480
1441 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 	B &	2 0	361 CCCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA
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3301 AGTCCTANAGCGAAGGAAGCATTTGAATATGCTGACTTGGAGAGGAGAACAAGAAGAAGGAGGAGAAGAAGAAGAAGA	3233 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCCTGGGATATAGA 3292 3181 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGT 3240	3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060	2821 AJAAGAACACTGACAGATAATTTGAAAGAAAAGCTCTTTCATTTATGAGGCAAGGT 2880	GAGATGTTCTTGGTCCATCAATGGCTTAGGCTCATTGATTCGGATGCCTTATGGC	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2580
RESULT 3 AX534938 LOCUS LOCUS DEFINITION Sequence 5 from Patent W002070696. ACCESSION AX534938 VERSION AX534938 VERSION AX534938.1 GI:25261482 CATHORIS ORGANISM Homo sapiens (human) CREPERENCE AUTHORS TITLE JOUNAL FEATURES BOURCE 1. 5895 bp DNA linear PAT 22-NOV-2002 AX534938.1 GI:25261482 CATHORISM Homo sapiens (human) CREPERENCE AUTHORS CATHORISM	4210 TCAG 4373 TCAG 4270 ATGG 4433 ATGG	Oy 4193 GITAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4252 Qy 4090 ATAGTGGATTACTATGAGCCAAGGAGACAGGTGAGAAGTTACAACTCTGAAGTGAAG Db 4253 ATAGTGGATTACTATGAGCCAAGGAGACAGGGGGTGAGAAGTTACAACTCTGAAGTGAAG Qy 4150 CTGTCCTCTGTGACCTTTGCAGTGATGCAGGGGTGAGAAGTTACAACTCTGAAGTGAAG 411	4013 GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTTCTCTGTAGGACAGTTAACCTA 4013 GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCTCTATGGAAGAAAGTT 3910 TTAAGTGGCCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG	Qy 3730 TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAATCAAGAAGCC 3789	Oy 3601 GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT 3651

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**4141 ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG
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                                                                            Query Match
Best Local Similarity
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AXS37612
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KSSMAVHSLEKSPSKTYIQLKTRDENIKVGSPFELLVVGGKRIKELSYMVVSRGQLVA
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YALLSHFLQFQTSEGIPINMILSRONSLGGFASTQDTTVALKALSFFAALMNTERIN
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GVELLEHCPSQVTVKAELKTASNLTVSVLEAGGVFEKGSFKILTLPSLDENSADEIY
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KTSLNILIKDPKSNLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQS
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KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI
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LSGFMVPSEAISLSETVKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDAS
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/db_xref="taxon:9606"
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